

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 26, 2005, 08:01:20 ; Search time 127.778 Seconds
(without alignments)
20.038 Million cell updates/sec

Title: US-10-053-669-1
Perfect score: 27
Sequence: 1 FGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum-DB-seq-length: 0
Maximum-DB-seq-length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :

1: uniprot_03.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	11	1	TKNA_PSEGU
2	27	100.0	11	1	TKN5_PSEGU
3	27	100.0	11	1	TKNA_CAVPO
4	27	100.0	11	1	TKNA_CHICK
5	27	100.0	11	1	TKNA_HORSE
6	27	100.0	11	1	TKNA_ONCMY
7	27	100.0	11	1	TKNA_SCYCA
8	27	100.0	45	1	061D93
9	27	100.0	69	1	VAT1_RHOBL
10	27	100.0	72	2	091454
11	27	100.0	74	2	081W27
12	27	100.0	76	2	086U06
13	27	100.0	82	2	06ECK5
14	27	100.0	87	2	086U07
15	27	100.0	96	2	086U08
16	27	100.0	99	2	086U09
17	27	100.0	100	2	09RD07
18	27	100.0	104	2	06ECK6
19	27	100.0	107	2	07VC12
20	27	100.0	107	2	06ECK8
21	27	100.0	108	2	08ES47
22	27	100.0	113	2	086U09
23	27	100.0	114	2	097947
24	27	100.0	115	2	TKN1_RABIT
25	27	100.0	116	2	0914V2
26	27	100.0	119	2	0940P5
27	27	100.0	124	2	09CGC7
28	27	100.0	129	1	TKN1_HUMAN
29	27	100.0	130	1	TKN1_BOVIN
30	27	100.0	130	1	TKN1_BOVIN
31	27	100.0	130	1	TKN1_MESAU

32	27	100.0	130	1	TKN1_MOUSE
33	27	100.0	130	1	TKN1_RAT
34	27	100.0	138	2	08RK61
35	27	100.0	138	2	08RK63
36	27	100.0	138	2	08RK75
37	27	100.0	147	2	0919H7
38	27	100.0	150	2	08TMB0
39	27	100.0	150	2	053986
40	27	100.0	150	2	069CB3
41	27	100.0	150	2	069CB7
42	27	100.0	150	2	075RU4
43	27	100.0	151	2	08MBL5
44	27	100.0	151	2	08MBM2
45	27	100.0	157	2	013092
46	27	100.0	166	2	08YYS0
47	27	100.0	170	2	09TX35
48	27	100.0	170	2	09TX35
49	27	100.0	173	2	07W9N5
50	27	100.0	179	2	09KANA
51	27	100.0	181	2	08LKM8
52	27	100.0	181	2	07WME0
53	27	100.0	208	2	07MTW2
54	27	100.0	224	2	08P1Q4
55	27	100.0	227	1	YP85_DEIRA
56	27	100.0	230	1	Y920_HELPJ
57	27	100.0	230	1	Y920_HELPJ
58	27	100.0	255	2	07WMT7
59	27	100.0	256	2	09UYK2
60	27	100.0	256	2	09K0J7
61	27	100.0	259	2	07ULC3
62	27	100.0	276	2	P72066
63	27	100.0	276	2	P72069
64	27	100.0	276	2	08R050
65	27	100.0	276	2	08LC64
66	27	100.0	278	2	085H03
67	27	100.0	285	2	08FY11
68	27	100.0	290	2	085XB3
69	27	100.0	291	2	08M6V3
70	27	100.0	292	2	028568
71	27	100.0	299	2	028888
72	27	100.0	299	2	028959
73	27	100.0	299	2	029935
74	27	100.0	301	2	08YJ86
75	27	100.0	311	2	06JC2P
76	27	100.0	312	2	068RK4
77	27	100.0	315	2	09P967
78	27	100.0	315	2	068RK6
79	27	100.0	319	1	Y189_MYCPN
80	27	100.0	319	2	0921P8
81	27	100.0	320	2	09B8K2
82	27	100.0	321	2	08BP56
83	27	100.0	322	2	08BP56
84	27	100.0	339	2	06ER27
85	27	100.0	339	2	07MBN1
86	27	100.0	345	2	09CYJ1
87	27	100.0	355	2	085GN7
88	27	100.0	355	2	08HDS7
89	27	100.0	355	2	08HDS7
90	27	100.0	355	2	09B5X2
91	27	100.0	355	2	09B5X2
92	27	100.0	355	2	09B5X3
93	27	100.0	355	2	09GBL2
94	27	100.0	355	2	09ML03
95	27	100.0	357	2	028862
96	27	100.0	375	2	09H1U3
97	27	100.0	380	2	057772
98	27	100.0	389	2	087NPS
99	27	100.0	397	1	FTSW_CVAPA
100	27	100.0	402	2	021056
101	27	100.0	402	2	09NE00
102	27	100.0	402	2	087YJ6
103	27	100.0	403	2	09XP03
104	27	100.0	403	2	09XP05

P41539	mus musculus
P06767	rattus norv
08K61	nitrosomona
08K63	nitrosospir
08K75	nitrosomona
09197	halocynthia
08TMB0	methanosarc
053986	nitrosomona
069CB3	uncultured
069CB7	uncultured
075RU4	uncultured
08MBL5	glytapanate
08MBM2	glytapanate
013092	homo sapien
08YYS0	anabaena sp
09TX35	disaster oc
07W9N5	borderella
09KANA	bacillus ha
08LKM8	medicago tr
07WME0	borderella
07MTW2	borderella
08P1Q4	porphyromon
YP85_DEIRA	xanthomonas
Y920_HELPJ	delnoccocus
025578	helicobacte
07WMT7	nitrosomona
09UYK2	neisseria m
09K0J7	neisseria m
07ULC3	rhodospirell
P72066	nitrosomona
P72069	nitrosomona
08R050	nitrosomona
08LC64	nitrosomona
085H03	cooperia on
08FY11	brucella su
085XB3	drosophila
08M6V3	belenois ja
028568	archaeoglob
028888	archaeoglob
028959	archaeoglob
029935	archaeoglob
08YJ86	brucella me
06JC2P	schizaphis
068RK4	schlechtend
09P967	tricholoma
068RK6	diuraphis n
P75262	mycoplasma
06W42	alcaligenes
0921P8	mus musculu
09B8K2	homo sapien
08BP56	oceanobacil
06ER27	coctesia acu
07MBN1	wolinnella s
09CYJ1	mus musculu
085GN7	carabus erw
08HDS7	carabus sic
08HDS7	carabus reg
09B5X2	ceroglossus
09B5X3	ceroglossus
09GBL2	carabus hae
09ML03	carabus art
028862	archaeoglob
09H1U3	thermoplasm
057772	pyrococcus
092614	libertia in
087NPS	vibriota para
P48280	caenorhabdi
021056	caenorhabdi
09NE00	pseudomonas
087YJ6	pholetecor
09XP03	glytapanate
09XP05	glytapanate

105	27	100.0	403	2	Q8KLX6	Q8KLX6 pseudomonas
106	27	100.0	404	2	Q9XNZ8	Q9XNZ8 apanteles n
107	27	100.0	404	2	Q8BP27	Q8BP27 pseudomonas
108	27	100.0	407	2	Q8H139	Q8H139 arbidopsis
109	27	100.0	408	2	Q9XP01	Q9XP01 dolichogeni
110	27	100.0	408	2	Q7VX47	Q7VX47 bordetella
111	27	100.0	408	2	Q7VLE6	Q7VLE6 bordetella
112	27	100.0	409	2	Q9XP06	Q9XP06 hypomicroga
113	27	100.0	409	2	Q9XP13	Q9XP13 cotesia mar
114	27	100.0	409	2	Q9XP15	Q9XP15 apanteles c
115	27	100.0	409	2	Q6LMI6	Q6LMI6 photobacter
116	27	100.0	409	2	Q87JM6	Q87JM6 vibrio para
117	27	100.0	409	2	Q8DS26	Q8DS26 vibrio vuln
118	27	100.0	410	2	Q6EB94	Q6EB94 leiscycta s
119	27	100.0	410	2	Q9XP00	Q9XP00 dolichogeni
120	27	100.0	410	2	Q9XP10	Q9XP10 microgastr
121	27	100.0	410	2	Q9XP11	Q9XP11 alphomelon
122	27	100.0	410	2	Q9XP14	Q9XP14 cotesia gryl
123	27	100.0	411	2	Q9XNZ7	Q9XNZ7 salton falc
124	27	100.0	411	2	Q9XP04	Q9XP04 glyptapante
125	27	100.0	411	2	Q7MHX0	Q7MHX0 vibrio vuln
126	27	100.0	416	1	PUR2_CLOAB	Q97390 clostridium
127	27	100.0	419	2	Q6XV78	Q6XV78 oncorhynch
128	27	100.0	420	2	Q69FH0	Q69FH0 salmo salar
129	27	100.0	421	2	Q6XNS2	Q6XNS2 rhodococcus
130	27	100.0	425	2	Q64DQ3	Q64DQ3 uncultured
131	27	100.0	426	1	PUR2_FUSNN	Q8REV7 fusobacteri
132	27	100.0	426	2	Q7PSQ4	Q7PSQ4 fusobacteri
133	27	100.0	429	2	Q6EF34	Q6EF34 cotesia acu
134	27	100.0	434	2	Q8BL78	Q8BL78 pseudomonas
135	27	100.0	436	2	Q92NM2	Q92NM2 thizobium m
136	27	100.0	437	2	Q6BXG4	Q6BXG4 debaryomyce
137	27	100.0	439	2	P92962	P92962 arbidopsis
138	27	100.0	444	2	Q6EF44	Q6EF44 cotesia acu
139	27	100.0	440	2	Q6EF34	Q6EF34 cotesia mel
140	27	100.0	444	2	Q6EF42	Q6EF42 cotesia acu
141	27	100.0	444	2	Q6EF45	Q6EF45 cotesia acu
142	27	100.0	455	2	Q6EF21	Q6EF21 cotesia acu
143	27	100.0	455	2	Q6EF23	Q6EF23 cotesia mel
144	27	100.0	456	2	Q6EF25	Q6EF25 cotesia big
145	27	100.0	456	2	Q6EF35	Q6EF35 cotesia mel
146	27	100.0	457	2	Q6EF23	Q6EF23 cotesia big
147	27	100.0	457	2	Q6EF24	Q6EF24 cotesia big
148	27	100.0	457	2	Q6EF26	Q6EF26 cotesia koe
149	27	100.0	497	2	Q6EF28	Q6EF28 cotesia mel
150	27	100.0	497	2	Q6EF29	Q6EF29 cotesia mel

ALIGNMENTS

RESULT 1
TKN4_PSECU STANDARD; PRT; 11 AA.
AC P42989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Substance P-like peptide I (PG-SP1).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCB1_Taxid=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.,
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guentheri.",
RL Peptides 11:299-304 (1990).

CC - FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: Skin.
CC - SIMILARITY: Belongs to the tachykinin family.
DR PIR; E60409; E60409. Tachy Neurokinin.
DR InterPro; IPR002040; Tachy Neurokinin.
DR PIR; F60409; F60409. Tachy Neurokinin.
DR SMART; SM00203; TK, 1.
DR PROSITE; PS00267; TACHYKININ, 1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing;
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
FT MOD RES 1 1
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1A87 CMC64;

Query Match 100.0%; Score 27; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRGLM 5
DB 7 FRGLM 11

RESULT 2
TKN5_PSECU STANDARD; PRT; 11 AA.

AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Substance P-like peptide II (PG-SP11).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCB1_Taxid=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.,
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guentheri.",
RL Peptides 11:299-304 (1990).
CC - FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: Skin.
CC - SIMILARITY: Belongs to the tachykinin family.
DR PIR; F60409; F60409.
DR InterPro; IPR002040; Tachy Neurokinin.
DR PIR; F60202; Tachykinin, 1.
DR PROSITE; PS00267; TACHYKININ, 1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing;
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
FT MOD RES 1 1
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1A57 CMC64;

Query Match 100.0%; Score 27; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRGLM 5
DB 7 FRGLM 11

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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:04:16 ; Search time 13.333 Seconds

(without alignments)
36.081 Million cell updates/sec

Title: US-10-053-669-1

Perfect score: 27
Sequence: 1 FFGIM 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 150 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	11	1 A60654	substance P - guin
2	27	100.0	11	1 SPHO	substance P - hots
3	27	100.0	11	2 JN0023	substance P - chic
4	27	100.0	11	2 S33300	probable substance
5	27	100.0	11	2 E60409	substance P-like p
6	27	100.0	11	2 E60409	substance P-like p
7	27	100.0	11	2 S23308	substance P - rain
8	27	100.0	63	2 JC2412	tachykinin gamma c
9	27	100.0	69	2 S04666	hypothetical prote
10	27	100.0	72	2 JC5455	preprotachykinin-A
11	27	100.0	72	2 I62742	tachykinin A gamma
12	27	100.0	97	2 S12958	tachykinin delta p
13	27	100.0	112	1 SPRTA	substance P alpha
14	27	100.0	115	1 SPRTB	substance P gamma
15	27	100.0	115	1 SPRTB	tachykinin 1 precu
16	27	100.0	116	2 C72232	hypothetical prote
17	27	100.0	124	2 B66771	hypothetical prote
18	27	100.0	129	1 SPHUB	neurokinin 1 precu
19	27	100.0	130	1 SPBOB	neurokinin 1 precu
20	27	100.0	130	1 SPRTB	substance P beta p
21	27	100.0	130	2 S47038	tachykinin 1 precu
22	27	100.0	130	2 I52526	neurokinin 1 precu
23	27	100.0	166	2 AG1931	hypothetical prote
24	27	100.0	173	2 B83931	hypothetical prote
25	27	100.0	230	1 H64634	conserved hypotet
26	27	100.0	230	2 F71879	hypothetical prote
27	27	100.0	234	2 F75254	conserved hypotet
28	27	100.0	256	2 D81181	conserved hypotet
29	27	100.0	256	2 C81925	probable sec-indep

30	27	100.0	299	2 F69422	ISA0963-4 transpos
31	27	100.0	299	2 H69462	ISA0963-6 transpos
32	27	100.0	299	2 E69413	ISA0963-3 transpos
33	27	100.0	299	2 E69288	ISA0963-2 transpos
34	27	100.0	301	2 AE3273	transporter, dne f
35	27	100.0	319	2 S73344	probable transport
36	27	100.0	357	2 A69426	ISA0963-5 transpos
37	27	100.0	380	2 E71218	hypothetical prote
38	27	100.0	397	2 T06957	probable cell divi
39	27	100.0	416	2 A97072	phosphoribosylam
40	27	100.0	439	2 T47713	proline transport
41	27	100.0	674	2 T20571	hypothetical prote
42	27	100.0	845	2 T25657	hypothetical prote
43	27	100.0	896	2 I45858	desmocollin - bov
44	27	100.0	1335	2 T17508	glycoprotein Vp260
45	25	92.6	79	2 AB3284	hypothetical prote
46	25	92.6	124	2 T36388	hypothetical prote
47	25	92.6	155	2 AB1545	B. subtilis ydck p
48	25	92.6	183	2 AG2944	hypothetical prote
49	25	92.6	187	2 T47342	hypothetical prote
50	25	92.6	207	2 E69124	cobalamin biosynth
51	25	92.6	207	2 C98338	hypothetical prote
52	25	92.6	258	2 A72266	hypothetical prote
53	25	92.6	266	2 A95114	hypothetical prote
54	25	92.6	266	2 B97983	seey protein homol
55	25	92.6	343	2 T01432	hypothetical prote
56	25	92.6	360	2 T27196	hypothetical prote
57	25	92.6	382	2 A70071	conserved hypotet
58	25	92.6	424	2 T44296	hypothetical prote
59	25	92.6	437	2 H81041	citrate transport
60	25	92.6	456	2 B90069	hypothetical prote
61	25	92.6	490	2 A35312	potassium channel
62	25	92.6	533	2 S62489	hypothetical prote
63	25	92.6	552	2 E69438	probable fatty-aci
64	25	92.6	553	2 T01416	seey protein homol
65	25	92.6	576	2 E86208	protein F2265.32 l
66	25	92.6	659	2 AB1293	ABC transporter (p
67	25	92.6	663	2 C95153	v-type sodium ATP
68	25	92.6	664	2 B53610	ncpl protein - Ent
69	25	92.6	676	2 E69394	H+-transporting AT
70	25	92.6	776	2 S43495	1ap4 protein - fls
71	25	92.6	801	2 G84370	heavy-metal transp
72	25	92.6	869	2 T32203	hypothetical prote
73	25	92.6	898	1 A44217	genome polypotein
74	25	92.6	3988	1 GNMVAV	genome polypotein
75	24	88.9	10	2 B49581	salokinin II - ye
76	24	88.9	10	2 A49581	salokinin I - ye
77	24	88.9	10	2 A24867	scylliorhizin I - s
78	24	88.9	10	2 B61033	renatachynkinin B -
79	24	88.9	11	2 S07203	uperolein - frog (
80	24	88.9	11	2 S07201	physalaemin - frog
81	24	88.9	11	2 A61033	renatachynkinin A -
82	24	88.9	51	2 S34506	photosystem II pro
83	24	88.9	53	2 H82739	hypothetical prote
84	24	88.9	66	2 C42529	B-ORF-B protein -
85	24	88.9	66	2 B36855	BEL protein - vari
86	24	88.9	66	2 T28601	hypothetical prote
87	24	88.9	75	2 G69221	hypothetical prote
88	24	88.9	80	2 D97909	hypothetical prote
89	24	88.9	87	2 T22923	hypothetical prote
90	24	88.9	93	1 S2305	ribosomal protein
91	24	88.9	104	2 F72590	hypothetical prote
92	24	88.9	114	2 E72600	hypothetical prote
93	24	88.9	129	2 F70728	hypothetical prote
94	24	88.9	133	2 S27488	probable membrane
95	24	88.9	144	2 G81043	hypothetical prote
96	24	88.9	155	1 JX0226	H+-exporting ATPas
97	24	88.9	155	1 JX0063	H+-exporting ATPas
98	24	88.9	156	1 JN0456	H+-exporting ATPas
99	24	88.9	156	2 A56680	H+-exporting ATPas
100	24	88.9	159	1 S42878	H+-exporting ATPas
101	24	88.9	159	2 S32544	H+-exporting ATPas
102	24	88.9	161	2 S32970	H+-exporting ATPas

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103      24      88.9      161      2      F82322      conserved hypothet
104      24      88.9      167      2      G90175      NADH dehydrogenase
105      24      88.9      169      2      D87294      ATP synthase F0, B
106      24      88.9      172      2      AE2283      hypothetical prote
107      24      88.9      178      2      JS0337      hypothetical 21k p
108      24      88.9      178      2      S07737      hypothetical prote
109      24      88.9      183      2      T44337      hypothetical prote
110      24      88.9      185      2      A64159      intracellular sept
111      24      88.9      189      2      C90592      hypothetical prote
112      24      88.9      197      2      E95011      hypothetical prote
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114      24      88.9      204      2      G86304      transcription regu
115      24      88.9      206      2      C70226      hypothetical prote
116      24      88.9      215      2      JX0244      pyroglyutamyl-pepti
117      24      88.9      215      2      S23432      pyroglyutamyl-pepti
118      24      88.9      217      2      C90525      ABC transporter at
119      24      88.9      217      2      F83840      stage II sporulat
120      24      88.9      218      2      S73526      MG364 homolog G12_
121      24      88.9      219      2      D70411      hypothetical prote
122      24      88.9      220      2      AD0225      probable amino-ac1
123      24      88.9      222      2      AB0750      probable ABC trans
124      24      88.9      222      2      A85809      probable transport
125      24      88.9      222      2      H90960      probable transport
126      24      88.9      222      2      C64355      probable ABC-type
127      24      88.9      224      2      C64240      mobilization prote
128      24      88.9      227      2      D86631      transposase of IS1
129      24      88.9      227      2      G86704      transposase of IS1
130      24      88.9      238      2      AE1704      hypothetical prote
131      24      88.9      238      2      AE1333      hypothetical prote
132      24      88.9      232      2      A84053      magnesium (Mg2+), c
133      24      88.9      233      2      A87601      hypothetical prote
134      24      88.9      234      2      B64544      triosephosphate is
135      24      88.9      235      2      T24882      hypothetical prote
136      24      88.9      239      2      JC7752      F-1ANA protein - h
137      24      88.9      244      2      A69502      conserved hypothet
138      24      88.9      255      2      AG1198      conserved hypothet
139      24      88.9      255      2      AE1556      conserved hypothet
140      24      88.9      264      2      A71367      probable holocytoe
141      24      88.9      264      2      T37551      hypothetical prote
142      24      88.9      265      2      A84937      undecaprenol kina
143      24      88.9      272      2      C86542      transposase of IS1
144      24      88.9      272      2      C86884      transposase of IS1
145      24      88.9      272      2      D86671      transposase of IS1
146      24      88.9      275      2      E75548      conserved hypothet
147      24      88.9      276      2      A49853      ammonia monooxygen
148      24      88.9      282      2      T19393      hypothetical prote
149      24      88.9      284      2      T33860      hypothetical prote
150      24      88.9      287      2      C84567      hypothetical prote

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ALIGNMENTS

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substance P - guinea pig
C/Species: Cavia porcellus (guinea pig)
C/Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C/Accession: A60654

```

```

R/Murphy, R.
Neuropeptides 14, 105-110, 1989

```

```

A/Title: Primary amino acid sequence of guinea-pig substance P.
A/Reference number: A60654; PMID:90044685; PMID:2478925

```

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A/Accession: A60654
A/Molecule type: protein

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A/Residues: 1-11 <MPR>
A/Cross-references: UNIPROT:P01290

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C/Superfamily: substance P precursor
C/Keywords: amidated carboxyl end; neuropeptide; tachykinin

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F/11/Modified site: amidated carboxyl end (Met) #status experimental

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Query Match      100.0%; Score 27; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3;

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      |||||
Db      7 FFGLM 11

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RESULT 2

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SPHO
substance P - horse

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```

C/Species: Equus caballus (domestic horse)
C/Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

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```

C/Accession: A01558
C/Study: R.O.; Tizetciak, A.; Lergier, W.

```

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A/Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.
A/Reference number: A01558

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A/Accession: A01558
A/Molecule type: protein

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A/Residues: 1-11 <STU>
A/Cross-references: UNIPROT:P01290

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C/Superfamily: substance P precursor
C/Keywords: amidated carboxyl end; hormone

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F/11/Modified site: amidated carboxyl end (Met) #status experimental

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Best Local Similarity 100.0%; Pred. No. 3;
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Qy      1 FFGLM 5
      |||||
Db      7 FFGLM 11

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RESULT 3

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substance P - chicken

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C/Species: Gallus gallus (chicken)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

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```

C/Accession: JN0023
R/Conlon, J.M.; Karsoulis, S.; Schmidt, W.E.; Thim, L.

```

```

Regul. Pept. 20, 171-180, 1988
A/Title: [Arg3]substance P and neurokinin A from chicken small intestine.

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A/Reference number: JN0023; PMID:88204263; PMID:2452461
A/Accession: JN0023

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A/Molecule type: protein
A/Residues: 1-11 <CON>

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A/Cross-references: UNIPROT:P19850
C/Superfamily: substance P precursor

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C/Keywords: amidated carboxyl end; tachykinin
F/11/Modified site: amidated carboxyl end (Met) #status predicted

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Best Local Similarity 100.0%; Pred. No. 3;
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Qy      1 FFGLM 5
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Db      7 FFGLM 11

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RESULT 4

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S33300
probable substance P - smaller spotted catshark

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C/Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

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```

C/Accession: S33300
C/Waugh, D.; Wang, Y.; Hazon, N.; Balmont, R.J.; Conlon, J.M.

```

```

Eur. J. Biochem. 214, 469-474, 1993
A/Title: Primary structures and biological activities of substance-P-related peptides fr

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A/Reference number: S33300; PMID:93292508; PMID:7685693
A/Accession: S33300
A/Molecule type: protein

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:05:47 ; Search time 124.444 Seconds
(without alignments)
16.775 Million cell updates/sec

Title: US-10-053-669-1
Perfect score: 27
Sequence: 1 FGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB-seq-length: 0
Maximum DB-seq-length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 150 summaries

Database :

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7: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
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9: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	27	100.0	5 16 US-10-688-741-3	Sequence 3, Appl1
5	27	100.0	5 17 US-10-805-881-1	Sequence 3, Appl1
6	27	100.0	5 16 US-10-805-881-1	Sequence 3, Appl1
7	27	100.0	5 16 US-10-720-039-3	Sequence 1, Appl1
8	27	100.0	5 17 US-10-497-628-15	Sequence 15, Appl1
9	27	100.0	5 20 US-11-066-697-604	Sequence 604, App
10	27	100.0	5 20 US-11-025-494-3	Sequence 3, Appl1
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Sequence 5, Appl1	Publication No. US20010051345A1
Sequence 8, Appl1	GENERAL INFORMATION:
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Sequence 5, Appl1	TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
Sequence 8, Appl1	TITLE OF INVENTION: for Disease Diagnosis
Sequence 2, Appl1	FILE REFERENCE: 1427001
Sequence 5, Appl1	CURRENT APPLICATION NUMBER: US/09/265,690C
Sequence 8, Appl1	CURRENT FILING DATE: 1999-03-10
Sequence 55, Appl1	NUMBER OF SEQ ID NOS: 4
Sequence 41, Appl1	SOFTWARE: PatentIn version 3.0
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Sequence 4, Appl1	Sequence 1, Application US/10053669
Sequence 10, Appl1	Publication No. US2003007658A1
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Sequence 4, Appl1	APPLICANT: Wellis, Ibert
Sequence 7, Appl1	TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
Sequence 10, Appl1	TITLE OF INVENTION: for Disease Diagnosis
Sequence 6, Appl1	FILE REFERENCE: N1427-005
Sequence 6, Appl1	CURRENT APPLICATION NUMBER: US/10/053,669
Sequence 6, Appl1	CURRENT FILING DATE: 2002-01-24
Sequence 2, Appl1	PRIOR APPLICATION NUMBER: 09/265,690
Sequence 58, Appl1	PRIOR FILING DATE: 1999-03-10
Sequence 23, Appl1	NUMBER OF SEQ ID NOS: 4
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Sequence 7, Appl1	ORGANISM: Homo sapiens
Sequence 60, Appl1	FEATURE:
Sequence 132100,	NAME/KEY: MOD_RES
Sequence 3, Appl1	LOCATION: (5)..(5)
Sequence 1454, Ap	OTHER INFORMATION: AMIDATION
Sequence 85, Appl1	US-10-053-669-1
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Sequence 109, App	Best Local Similarity 100.0%; Score 27; DB 14; Length 5;
Sequence 1495, Ap	Best Local Similarity 100.0%; Pred. NO. 1.7e+06;
Sequence 1496, Ap	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Sequence 365204,	1 FFGLM 5
Sequence 22, Appl1	
Sequence 20, Appl1	Db
Sequence 27, Appl1	1 FFGLM 5
Sequence 29, Appl1	RESULT 3
Sequence 288333,	US-10-134-187-3

RESULT 1
US-09-265-690C-1

US-09-265-690C-1

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 26, 2005, 08:04:31 : Search time 33.333 Seconds
(without alignments)
11.197 Million cell updates/sec

Title: US-10-053-669-1
Perfect score: 27
Sequence: 1 PFCGM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

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6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	27	100.0	5	1	US-08-225-474-2
3	27	100.0	5	2	US-07-737-371E-6
4	27	100.0	5	3	US-09-265-690C-1
5	27	100.0	6	1	US-07-934-553-3
6	27	100.0	6	1	US-08-225-474-3
7	27	100.0	6	2	US-08-430-238-15
8	27	100.0	6	2	US-07-737-371E-5
9	27	100.0	6	3	US-09-317-125-5
10	27	100.0	6	4	US-09-428-692-39
11	27	100.0	6	4	US-09-428-692-41
12	27	100.0	7	1	US-07-712-8288-7
13	27	100.0	7	2	US-07-737-371E-8
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149	27	100.0	13	4	US-09-922-098F-51	Sequence 51, Appl1
150	27	100.0	13	4	US-09-922-098F-52	Sequence 52, Appl1

ALIGNMENTS

RESULT 1
US-07-934-553-2
Sequence 2, Application US/07934553
Patent No. 5314690
GENERAL INFORMATION:
APPLICANT: PATTERSON, ROY
TITLE OF INVENTION: HARRIS, KATHLEEN E
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSER: TILTON, FALLON, LUNGKUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,553
FILING DATE: 19920821
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: FENTRESS, SUSAN B
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9033CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/456-8000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-934-553-2
Query Match 100.0%; Score 27; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FPGM 5
Db 1 FPGM 5
RESULT 2
US-08-225-474-2
Sequence 2, Application US/08225474
Patent No. 5560915
GENERAL INFORMATION:
APPLICANT: PATTERSON, ROY
TITLE OF INVENTION: HARRIS, KATHLEEN E
TITLE OF INVENTION: Method and Composition for Treating
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSER: TILTON, FALLON, LUNGKUS & CHESTNUT
STREET: 100 S. Wacker Drive, Suite 960
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,474
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,553
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.
REGISTRATION NUMBER: 16,926
REFERENCE/DOCKET NUMBER: NU 9033-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)-456-8000

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OM protein - protein search, using bw model

Run on: October 26, 2005, 08:00:50 ; Search time 72.222 Seconds
(without alignments)
26.776 Million cell updates/sec

Title: US-10-053-669-1
Perfect score: 27
Sequence: 1 FGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB-seq length: 0
Maximum DB-seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 150 summaries

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2: genesegp1990s:.*
3: genesegp2000s:.*
4: genesegp2001s:.*
5: genesegp2002s:.*
6: genesegp2003as:.*
7: genesegp2003bs:.*
8: genesegp2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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8	27	100.0	5	2 AAR54548	Aar54548 Cholecytc
9	27	100.0	5	2 AAR41687	Aar41687 Tetrapt
10	27	100.0	5	2 AAR99643	Aar99643 Substance
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19	27	100.0	5	8 ADF92530	Adf92530 Substance
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24	27	100.0	6	1 AAP50632	Aap50632 Substance
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27	27	100.0	6	2 AAR21959	Aar21959 Substance
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74	27	100.0	9	4 AAB91369	Aab91369 Tachykin
75	27	100.0	9	4 AAG99348	Aag99348 Aclycal
76	27	100.0	9	7 ADR92528	Adr92528 Substance
77	27	100.0	9	8 ADN95076	Adn95076 Mammalian
78	27	100.0	10	1 AAP50633	Aap50633 Substance
79	27	100.0	10	2 AAR21933	Aar21933 Substance
80	27	100.0	10	2 AAR65181	Aar65181 S. cerevi
81	27	100.0	10	2 AAY06939	Aay06939 Substance
82	27	100.0	10	2 AAW92663	Aaw92663 Human tac
83	27	100.0	10	4 AAB91445	Aab91445 Tachykin
84	27	100.0	10	4 AAG99347	Aag99347 Aclycal
85	27	100.0	10	4 AAG64746	Aag64746 Substance
86	27	100.0	10	8 ADN12181	Adn12181 Amino aci
87	27	100.0	10	8 ADN27868	Adn27868 Trichomon
88	27	100.0	11	1 AAP61480	Aap61480 Sequence
89	27	100.0	11	1 AAP80332	Aap80332 Sequence
90	27	100.0	11	2 AAR11854	Aar11854 Undecapep
91	27	100.0	11	2 AAR13162	Aar13162 Sialic ac
92	27	100.0	11	2 AAR28442	Aar28442 Substance
93	27	100.0	11	2 AAR21942	Aar21942 Substance
94	27	100.0	11	2 AAR21962	Aar21962 Substance
95	27	100.0	11	2 AAR21945	Aar21945 Substance
96	27	100.0	11	2 AAR21963	Aar21963 Substance
97	27	100.0	11	2 AAR21949	Aar21949 Substance
98	27	100.0	11	2 AAR21951	Aar21951 Substance

99	27	100.0	11	2	AAK21946	Aar21946 Substance
100	27	100.0	11	2	AAK21964	Aar21964 Substance
101	27	100.0	11	2	AAK21970	Aar21970 Cyclic su
102	27	100.0	11	2	AAK21938	Aar21938 Substance
103	27	100.0	11	2	AAK21941	Aar21941 Substance
104	27	100.0	11	2	AAK21954	Aar21954 Substance
105	27	100.0	11	2	AAK22646	Aar22646 Substance
106	27	100.0	11	2	AAK85243	Aar85243 Substance
107	27	100.0	11	2	AAK77310	Aar77310 Substance
108	27	100.0	11	2	AAK33181	Aar33181 Mono-DTPA
109	27	100.0	11	2	AAK33180	Aar33180 Mono-DTPA
110	27	100.0	11	2	AAK04616	Aar04616 Substance
111	27	100.0	11	2	AAK79775	Aar79775 Substance
112	27	100.0	11	2	AAK42973	Aar42973 Substrate
113	27	100.0	11	2	AAK79663	Aar79663 Substance
114	27	100.0	11	2	AAK79662	Aar79662 Substance
115	27	100.0	11	2	AAK92679	Aar92679 Human tac
116	27	100.0	11	2	AAK92676	Aar92676 Human tac
117	27	100.0	11	2	AAK92720	Aar92720 Human tac
118	27	100.0	11	2	AAK92673	Aar92673 Human tac
119	27	100.0	11	2	AAK92708	Aar92708 Human tac
120	27	100.0	11	2	AAK92731	Aar92731 Human tac
121	27	100.0	11	2	AAK92670	Aar92670 Human tac
122	27	100.0	11	2	AAK92689	Aar92689 Human tac
123	27	100.0	11	2	AAK92715	Aar92715 Human tac
124	27	100.0	11	2	AAK92719	Aar92719 Human tac
125	27	100.0	11	2	AAK92680	Aar92680 Human tac
126	27	100.0	11	2	AAK92681	Aar92681 Human tac
127	27	100.0	11	2	AAK92672	Aar92672 Human tac
128	27	100.0	11	2	AAK92690	Aar92690 Human tac
129	27	100.0	11	2	AAK30985	Aar30985 Non-cross
130	27	100.0	11	2	AAK03156	Aar03156 Substance
131	27	100.0	11	2	AD124903	Ad124903 Substance
132	27	100.0	11	3	AAK23027	Aak23027 Human/rat
133	27	100.0	11	3	AAK18483	Aak18483 Peptide s
134	27	100.0	11	3	AAK32382	Aay32382 Cell diffe
135	27	100.0	11	3	AAK06260	Aab06260 Substance
136	27	100.0	11	3	AAK08614	Aab08614 Peptide 1
137	27	100.0	11	4	AAK50311	Aab50311 Pevain pe
138	27	100.0	11	4	AAK50312	Aab50312 Pevain pe
139	27	100.0	11	4	AAK50306	Aab50306 Substance
140	27	100.0	11	4	AAK50316	Aab50316 Pevain pe
141	27	100.0	11	4	AAK50544	Aab50544 Prolyl en
142	27	100.0	11	4	AAK91450	Aab91450 Tachykinl
143	27	100.0	11	4	AAK91438	Aab91438 Tachykinl
144	27	100.0	11	4	AAK91449	Aab91449 Tachykinl
145	27	100.0	11	4	AAK91402	Aab91402 Tachykinl
146	27	100.0	11	4	AAK91436	Aab91436 Tachykinl
147	27	100.0	11	4	AAK99358	Aag99358 ATT-short
148	27	100.0	11	4	AAK99354	Aag99354 Substance
149	27	100.0	11	4	AAK99337	Aag99337 Human aty
150	27	100.0	11	4	AAU07298	Aau07298 Substance

ALIGNMENTS

RESULT 1
AAK33009 standard; peptide; 5 AA.
ID AAK33009;
AC AAK33009;
XX 25-MAR-2003 (revised)
DT 02-APR-1993 (first entry)
XX Alpha-substituted short peptide.
DE CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
XX improved bioavailability.
KM Synthetic.
XX

PH	Key	Location/Qualifiers
FT	Modified-site	4 /note= "alpha-Me-Leu"
FT	Modified-site	5 /note= "Met-NH2"
XX	MO9219254-A1.	
XX	12-NOV-1992.	
XX	15-APR-1992;	92WO-US003119.
XX	24-APR-1991;	91US-00690755.
PR	20-MAR-1992;	92US-00852086.
XX	(WARN) WARNER LAMBERT CO.	
XX	Horwell DC, Hughes J, Richardson RS, Howson W;	
XX	WPI; 1992-398522/48.	
DR	New alpha-substd. polypeptide are e.g. selective receptor ligands - for	
XX	treating inflammation, pain, stroke, ulcers, hypertension, heart failure,	
PT	depression, cancer, asthma, psychosis, arthritis, etc.	
XX	Claim 3; Page 41; 46pp; English.	
PS	The peptide is a specifically claimed example of a group of generically	
XX	claimed mono-, di-, tri-, tetra- and penta-peptides which include a	
CC	substituent on an alpha-C atom in the chain. Such substitution may modify	
CC	the bioavailability, stability or absorbability of the peptide and hence	
CC	may improve the activity of the peptide as a drug. Depending on the	
CC	nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic	
CC	peptide, etc.), the modified peptides are variously useful for treating	
CC	obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,	
CC	addictive drug withdrawal symptoms, hypertension, heart failure,	
CC	cognition or memory disorders, spasticity, depression, diabetes, cancer,	
CC	asthma, bladder dysfunction, psychosis and arthritis; and as	
CC	contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on	
CC	25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR	
CC	field.) (Updated on 25-MAR-2003 to correct PI field.)	
XX	Sequence 5 AA;	
SQ	Query Match	100.0%; Score 27; DB 2; Length 5;
	Best Local Similarity	100.0%; Pred. No. 1.8e+06;
	Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 FRGLM 5	
DB	1 FRGLM 5	
RESULT 2		
AAK33008		
ID	AAK33008 standard; peptide; 5 AA.	
XX		
AC	AAK33008;	
XX		
DT	25-MAR-2003 (revised)	
DT	02-APR-1993 (first entry)	
XX		
DE	Alpha-substituted short peptide.	
XX		
DE	CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;	
KM	improved bioavailability.	
KW		
XX		
OS	Synthetic.	
XX		
Key	Location/Qualifiers	
FT	Modified-site	2 /note= "alpha-Me-Phe"
FT	Modified-site	5

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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:12:17 ; Search time 124.444 Seconds
(without alignments)
20.575 Million cell updates/sec

Title: us-10-053-669-1
Perfect score: 27
Sequence: 1 FGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3223

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Listing first 150 summaries

Database :

1: uniprot_03.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	11	1	TKN4_PSEGU
2	27	100.0	11	1	TKN5_PSEGU
3	27	100.0	11	1	TKNA_CAYPO
4	27	100.0	11	1	TKNA_CHICK
5	27	100.0	11	1	TKNA_HORSE
6	27	100.0	11	1	TKNA_ONCMY
7	27	100.0	11	1	TKNA_SCYCA
8	24	88.9	10	1	TKN1_SCYCA
9	24	88.9	10	1	TKN5_RANCA
10	24	88.9	10	1	TKS1_AEDAE
11	24	88.9	10	1	TKS2_AEDAE
12	24	88.9	11	1	TKN1_UPEIN
13	24	88.9	11	1	TKN2_UPEIN
14	24	88.9	11	1	TKN2_UPEIN
15	24	88.9	11	1	TKNA_RANCA
16	24	88.9	11	1	TKNA_RANCA
17	24	88.9	11	1	TKN1_PHYRU
18	24	88.9	11	1	TKN1_PHYRU
19	24	88.9	11	1	TKN1_PHYRU
20	24	88.9	11	1	TKN1_PHYRU
21	24	88.9	11	1	TKN1_PHYRU
22	24	88.9	11	1	TKN1_PHYRU
23	24	88.9	11	1	TKN1_PHYRU
24	24	88.9	11	1	TKN1_PHYRU
25	24	88.9	11	1	TKN1_PHYRU
26	24	88.9	11	1	TKN1_PHYRU
27	24	88.9	11	1	TKN1_PHYRU
28	24	88.9	11	1	TKN1_PHYRU
29	24	88.9	11	1	TKN1_PHYRU
30	24	88.9	11	1	TKN1_PHYRU
31	24	88.9	11	1	TKN1_PHYRU

32	20	74.1	11	1	TKN1_PSEGU	P42986 pseudophryn
33	20	74.1	11	1	TKN2_PSEGU	P42987 pseudophryn
34	20	74.1	11	1	TKN3_PSEGU	P42988 pseudophryn
35	18	66.7	9	2	O30750	O30750 erwina amy
36	18	66.7	10	1	TKU2_UREBUN	P40752 urechis uni
37	18	66.7	11	2	Q9UC46	Q9UC46 homo sapien
38	17	63.0	10	2	PAP1_PARMA	P81863 paridachirus
39	17	63.0	10	2	Q6UL57	Q6UL57 neiseeria g
40	17	63.0	11	2	O65907	O65907 silene ajan
41	16	59.3	5	1	ALL4_CARMA	P81817 carcinus ma
42	16	59.3	7	1	ALL2_CARMA	P81805 carcinus ma
43	16	59.3	7	1	ALL3_CARMA	P81806 carcinus ma
44	16	59.3	7	1	ALL4_CARMA	P81807 carcinus ma
45	16	59.3	7	1	ALL5_CARMA	P81808 carcinus ma
46	16	59.3	7	1	ALL7_CARMA	P82158 cydia pomon
47	16	59.3	8	1	ALL2_CARMA	P81815 carcinus ma
48	16	59.3	8	1	ALL15_CARMA	P81818 carcinus ma
49	16	59.3	8	1	ALL17_CARMA	P81820 carcinus ma
50	16	59.3	8	1	ALL18_CARMA	P81821 carcinus ma
51	16	59.3	8	1	ALL19_CARMA	P82152 cydia pomon
52	16	59.3	8	1	ALL3_CYPDO	P82154 cydia pomon
53	16	59.3	8	1	ALL4_CYPDO	P41840 calliphora
54	16	59.3	8	1	ALL4_CYPDO	P82155 cydia pomon
55	16	59.3	8	1	ALL5_CYPDO	P82156 cydia pomon
56	16	59.3	8	1	ALL6_CYPDO	P82157 cydia pomon
57	16	59.3	8	1	ALL7_CARMA	P81809 carcinus ma
58	16	59.3	8	1	ALL8_CARMA	P81811 carcinus ma
59	16	59.3	8	1	ALL9_CARMA	P81812 carcinus ma
60	16	59.3	9	1	ALL10_CARMA	P81813 carcinus ma
61	16	59.3	9	1	ALL11_CARMA	P81814 carcinus ma
62	16	59.3	9	1	TKC1_CALVO	P41513 calliphora
63	16	59.3	9	1	TKC1_LOCOMI	P16223 locusta mig
64	16	59.3	9	2	O7S3Z9	O7S3Z9 neurospora
65	16	59.3	10	1	ALL9_CARMA	P81822 carcinus ma
66	16	59.3	10	1	TKL2_LOCOMI	P16224 locusta mig
67	16	59.3	10	1	TKL3_LOCOMI	P30249 locusta mig
68	16	59.3	10	2	O7M3T9	O7M3T9 tritpneustes
69	16	59.3	10	2	O7M4B9	O7M4B9 heterocentr
70	16	59.3	10	2	O8GDC0	O8GDC0 escherichia
71	15	55.6	8	2	O09258	O09258 synchococc
72	15	55.6	10	2	O35013	O35013 meloidogyne
73	15	55.6	10	2	O7M278	O7M278 tritcolum tu
74	15	55.6	10	2	O52837	O52837 rhizobium 1
75	14	51.9	8	1	ALL5_CALVO	P41841 calliphora
76	14	51.9	8	2	O40530	O40530 nicotiana t
77	14	51.9	9	2	TRP4_LEUMA	P81736 leucophaea
78	14	51.9	9	2	O7M3L3	O7M3L3 penaeus van
79	14	51.9	10	2	O7SMD5	O7SMD5 homo sapien
80	14	51.9	11	2	O9R446	O9R446 neiseeria g
81	13	48.1	8	1	ALL6_CARMA	O9R446 neiseeria g
82	13	48.1	8	2	O9R446	O9R446 neiseeria g
83	13	48.1	8	2	O7M032	O7M032 ratius norv
84	13	48.1	10	1	GONI_ALIMI	P37041 alligator m
85	13	48.1	10	1	TRP8_LEUMA	P81740 leucophaea
86	13	48.1	10	2	O7M4X1	O7M4X1 basidiobolu
87	13	48.1	10	2	O9NP06	O9NP06 homo sapien
88	13	48.1	11	2	O7S183	O7S183 neurospora
89	13	48.1	11	2	O9UR55	O9UR55 pichia angu
90	13	48.1	11	2	O6U255	O6U255 litoria a
91	13	48.1	11	2	O6K446	O6K446 oryctolagus
92	13	48.1	11	2	O6LDB5	O6LDB5 mus sp. gen
93	13	48.1	11	2	O7M0E2	O7M0E2 mus sp. gen
94	13	48.1	11	2	O6R205	O6R205 oncorhynch
95	12	44.4	4	1	FFKA_AINTEL	P58705 anthopleura
96	12	44.4	4	1	OCP1_OCTMI	P58648 octopus min
97	12	44.4	5	1	PAP2_PARMA	P81864 paridachirus
98	12	44.4	5	1	REI1_LITRU	P82070 litoria rub
99	12	44.4	5	1	REI2_LITRU	P82071 litoria rub
100	12	44.4	5	1	REI3_LITRU	P82072 litoria rub
101	12	44.4	5	1	REI4_LITRU	P82073 litoria rub
102	12	44.4	5	1	UC22_MAIZE	P80628 zea mays (m
103	12	44.4	6	1	FARP_MONEX	P41966 monstera ex
104	12	44.4	8	1	CCRN_DASVI	P68125 dasyurus vl

105	12	44.4	8	1	CCRN_MACEU	P68126	macropus eu
106	12	44.4	8	1	DYS1_LIMIN	P82079	limodysnat
107	12	44.4	8	2	013591	013591	saccharomyc
108	12	44.4	8	2	09P0K3	09P0K3	homo sapien
109	12	44.4	8	2	06R408	06R408	bubalus bub
110	12	44.4	8	2	09T4Y2	09T4Y2	asterina pe
111	12	44.4	8	2	09T002	09T002	terranacos
112	12	44.4	8	2	07X139	07X139	staphylococ
113	12	44.4	8	2	07X145	07X145	staphylococ
114	12	44.4	8	2	07ZP11	07ZP11	human immun
115	12	44.4	9	1	FIIBB_ERYPA	P19346	erythrocebu
116	12	44.4	9	1	FIIBB_THRGE	P19342	theropithec
117	12	44.4	9	1	RE42_LITRU	P82075	litorea rub
118	12	44.4	9	2	099887	099887	homo sapien
119	12	44.4	9	2	07R806	07R806	plasmodium
120	12	44.4	9	2	08MJN1	08MJN1	cebuella py
121	12	44.4	9	2	08MJN2	08MJN2	calithrix
122	12	44.4	9	2	08MJN3	08MJN3	callimico g
123	12	44.4	9	2	08MJN4	08MJN4	leontopithec
124	12	44.4	9	2	08MJN5	08MJN5	sagunus fu
125	12	44.4	9	2	08MJN6	08MJN6	actus azara
126	12	44.4	9	2	08MJN7	08MJN7	saimiri sci
127	12	44.4	9	2	08MJN8	08MJN8	cebus apell
128	12	44.4	9	2	08MJN9	08MJN9	ateles fusc
129	12	44.4	9	2	08MJT7	08MJT7	eulemur ful
130	12	44.4	9	2	08MJT8	08MJT8	eulemur ful
131	12	44.4	9	2	07M394	07M394	sus scrofa
132	12	44.4	9	2	0691D6	0691D6	anolis sagr
133	12	44.4	9	2	06XBN2	06XBN2	vicia pach
134	12	44.4	9	2	085G96	085G96	pyrrobrum
135	12	44.4	9	2	09G036	09G036	juncus efu
136	12	44.4	9	2	09MMF4	09MMF4	buteo rufin
137	12	44.4	9	2	09MMG9	09MMG9	buteo buteo
138	12	44.4	9	2	09T688	09T688	gecko gecko
139	12	44.4	9	2	P82440	P82440	nicotiana t
140	12	44.4	9	2	09AXH8	09AXH8	mesembryant
141	12	44.4	9	2	07M139	07M139	unidentifie
142	12	44.4	9	2	06TF34	06TF34	rattus norv
143	12	44.4	9	2	071U00	071U00	rattus norv
144	12	44.4	9	2	06T1E2	06T1E2	sars corona
145	12	44.4	9	2	07LZT5	07LZT5	rana escul
146	12	44.4	9	2	07ZP19	07ZP19	human immun
147	12	44.4	9	2	07ZP13	07ZP13	human immun
148	12	44.4	9	2	07ZP05	07ZP05	human immun
149	12	44.4	9	2	07ZP07	07ZP07	human immun
150	12	44.4	9	2	07ZPK1	07ZPK1	human immun

ALIGNMENTS

RESULT 1
TKN4_PSECU STANDARD; PRT; 11 AA.
AC P42989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Substance P-like peptide I (PG-SP1).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
NCBI_TaxID=30349;
RN [1]
RP TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;
RA Simmaco M., Severini C., de Biase D., Barra D., Boesa F.,
RT Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RT Peptides 11:299-304(1990).

CC - FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: Skin.
CC - SIMILARITY: Belongs to the tachykinin family.
DR PIR; E60409; E60409. Tachy Neurokinin.
DR InterPro; IPR002040; Tachy Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing;
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
FT MOD RES 1 1
FT MOD RES 11 1
FT MOD RES 11 1
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1A87 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRGLM 5
Db 7 FRGLM 11

RESULT 2
TKN5_PSECU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Substance P-like peptide II (PG-SP1I).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
NCBI_TaxID=30349;
RN [1]
RP TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;
RA Simmaco M., Severini C., de Biase D., Barra D., Boesa F.,
RT Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RT Peptides 11:299-304(1990).

CC - FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: Skin.
CC - SIMILARITY: Belongs to the tachykinin family.
DR PIR; F60409; F60409. Tachy Neurokinin.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.

KW Amidation; Amphibian defense peptide; Direct protein sequencing;
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
FT MOD RES 1 1
FT MOD RES 11 1
FT MOD RES 11 1
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1A57 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRGLM 5
Db 7 FRGLM 11

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 26, 2005, 08:12:37 ; Search time 25.5556 Seconds
(without alignments)
18.825 Million cell updates/sec

Title: UB-10-053-669-1
Sequence: 1 PFGIM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1328

Minimum DB-seq-length=0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :
1: PIR 79.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	11	1 A60654	substance P - guin
2	27	100.0	11	1 SPHO	substance P - hois
3	27	100.0	11	1 JN0023	substance P - chic
4	27	100.0	11	2 S33300	probable substance
5	27	100.0	11	2 E60409	substance P-like P
6	27	100.0	11	2 F60409	substance P-like P
7	27	100.0	11	2 S23308	substance P - rain
8	24	88.9	10	2 B49581	galactin II - ye
9	24	88.9	10	2 A49581	galactin I - ye
10	24	88.9	10	2 A24867	scyllokinin I - s
11	24	88.9	10	2 B61033	renatechkinin B -
12	24	88.9	11	2 S07203	urotelin - frog (
13	24	88.9	11	2 S07201	physalaemin - frog
14	24	88.9	11	2 A61033	renatechkinin A -
15	21	77.8	10	2 S07202	phyllomedulin - tw
16	21	77.8	10	2 C61033	renatechkinin C -
17	21	77.8	10	2 S27178	neurokinin A-relat
18	21	77.8	11	1 E00CC	eledosin - musky
19	21	77.8	11	1 E00CC	eledosin - curled
20	21	77.8	11	1 S23306	substance P - Acta
21	20	74.1	10	1 SPPGNK	neurokinin K - pig
22	20	74.1	10	2 JN0024	neurokinin A - chi
23	20	74.1	10	2 S23307	neurokinin A - rai
24	20	74.1	10	2 S23307	neurokinin A - rai
25	20	74.1	11	2 B60409	kaesinin-like pept
26	20	74.1	11	2 B60409	kaesinin-like pept
27	20	74.1	11	2 D60409	kaesinin-like pept
28	18	66.7	5	2 PT0278	ig heavy chain CRD
29	18	66.7	10	2 PH0807	T-cell receptor al

30	17	63.0	11	2 PT0249	Ig heavy chain CRD
31	16	59.3	8	2 D47393	neuropeptide calia
32	16	59.3	10	1 ECLQ3M	tachykinin I - mig
33	16	59.3	10	1 ECLQ3M	tachykinin III - m
34	16	59.3	10	2 P60527	sperm-activating p
35	16	59.3	10	2 B60589	sperm-activating p
36	16	59.3	11	1 ECLQ2M	tachykinin II - ml
37	15	55.6	7	2 S33932	Ig mu chain D regi
38	15	55.6	10	2 S06964	hypothetical prote
39	15	55.6	10	2 S19296	16k protein - poul
40	14	51.9	5	2 A44955	alkanal monooxygen
41	14	51.9	8	2 E47393	neuropeptide calia
42	14	51.9	9	2 PD0027	pev-tachykinin - p
43	13	48.1	8	2 PH1618	Ig H chain V-D-J r
44	13	48.1	8	2 PC4373	telomeric and tetr
45	13	48.1	9	2 PT0225	Ig heavy chain CDR
46	13	48.1	9	2 PH1591	Ig H chain V-D-J r
47	13	48.1	10	1 RHPG	gonadolibetin - pl
48	13	48.1	10	1 RSHG	gonadolibetin - sh
49	13	48.1	10	1 RHAQ1	gonadolibetin I -
50	13	48.1	10	2 PT0230	Ig heavy chain CDR
51	13	48.1	10	2 PT0310	Ig heavy chain CRD
52	13	48.1	10	2 PH1633	Ig H chain V-D-J r
53	13	48.1	10	2 S68033	cytochrome P450 1A
54	13	48.1	10	2 A59173	nuclease Bnl (EC 3
55	13	48.1	11	2 A57458	gene Gax protein - c
56	13	48.1	11	4 PC2124	aminotransferase c
57	12	44.4	4	2 J01373	neuropeptide Antho
58	12	44.4	6	2 A43129	neuropeptide GNPFR
59	12	44.4	7	1 A61324	dermorphin - Rohde
60	12	44.4	7	2 S36662	dermorphin (Iys-7)
61	12	44.4	7	2 I40504	hypothetical prote
62	12	44.4	8	2 P00012	cholecystokinin -
63	12	44.4	8	2 A43001	cholecystokinin -
64	12	44.4	8	2 A42057	fibroblast growth
65	12	44.4	8	2 PH0803	T-cell receptor al
66	12	44.4	8	2 S11078	glucose-6-phosphat
67	12	44.4	8	2 T13818	cytochrome oxidase
68	12	44.4	9	2 D24180	fibronogen beta ch
69	12	44.4	9	2 F28854	fibronopeptide B -
70	12	44.4	9	2 PT0285	Ig heavy chain CRD
71	12	44.4	9	2 PT0315	Ig heavy chain CRD
72	12	44.4	9	2 PH0942	T-cell receptor be
73	12	44.4	9	2 G58502	kidney and bladder
74	12	44.4	9	2 PT0080	60K Ca binding pro
75	12	44.4	9	2 PC7074	translacion elonga
76	12	44.4	9	2 S15850	vitamin D3 26-mono
77	12	44.4	10	1 ECLQ4M	tachykinin IV - ml
78	12	44.4	10	2 A13687	caerulein-like pep
79	12	44.4	10	2 S28305	lectin GNL2 alpha
80	12	44.4	10	2 A27617	triase-phosphate i
81	12	44.4	10	2 PN0165	triase-phosphate i
82	12	44.4	10	2 A58365	neuropeptide FRFa
83	12	44.4	10	2 T13838	cytochrome-c oxida
84	12	44.4	10	2 T13976	cytochrome-c oxida
85	12	44.4	10	2 T17057	cytochrome-c oxida
86	12	44.4	10	2 T12303	cytochrome-c oxida
87	12	44.4	10	2 T14019	cytochrome-c oxida
88	12	44.4	10	2 T17060	cytochrome-c oxida
89	12	44.4	10	2 T14043	cytochrome-c oxida
90	12	44.4	10	2 T14054	cytochrome-c oxida
91	12	44.4	10	2 T17066	cytochrome-c oxida
92	12	44.4	10	2 T17069	cytochrome-c oxida
93	12	44.4	10	2 T12308	cytochrome-c oxida
94	12	44.4	10	2 T17072	cytochrome-c oxida
95	12	44.4	10	2 T12312	cytochrome-c oxida
96	12	44.4	10	2 T12316	cytochrome-c oxida
97	12	44.4	10	2 T12321	cytochrome-c oxida
98	12	44.4	10	2 T14219	cytochrome-c oxida
99	12	44.4	11	2 PT0250	Ig heavy chain CRD
100	12	44.4	11	2 S57575	T-cell receptor V-
101	12	44.4	11	2 A54348	N-acetylglucosamin
102	12	44.4	11	2 C58501	42K bile stone pro

103	12	44.4	11	2	A44755	20alpha-hydroxyste
104	12	44.4	11	2	S69349	neuropeptide Ffam1
105	11	40.7	5	2	A61445	Met-enkephalin - b
106	11	40.7	7	2	A60224	Met-enkephalin-Arg
107	11	40.7	8	2	PC4372	telomeric and tetr
108	11	40.7	9	2	E28854	fibrinopeptide B-
109	11	40.7	9	2	A11497	transaldolase (EC
110	11	40.7	9	2	D57444	neuropeptide Grb-A
111	11	40.7	9	2	D44787	callifmrfamide 13
112	11	40.7	9	2	D49406	bone gla protein -
113	11	40.7	10	1	GMROI2	leucosulfakinin-II
114	11	40.7	10	2	B60556	leucosulfakinin-II
115	11	40.7	11	1	GMROI	leucosulfakinin II
116	11	40.7	11	2	A40693	transgelin - sheep
117	11	40.7	11	2	A60656	perisulfakinin - A
118	11	40.7	11	2	D61033	ranachykinin D -
119	11	37.0	4	2	PT0240	Ig heavy chain CRD
120	10	37.0	4	2	A53284	T-cell receptor be
121	10	37.0	5	2	G44817	27.5 kDa structura
122	10	37.0	5	2	I44817	27.5K structural p
123	10	37.0	5	2	E44817	28.5K structural p
124	10	37.0	5	2	C44817	28K structural pro
125	10	37.0	5	2	A44817	collagen alpha 1(I
126	10	37.0	6	2	B56979	T-cell receptor be
127	10	37.0	6	2	PT0643	T-cell receptor be
128	10	37.0	6	2	PT0718	T-cell receptor be
129	10	37.0	6	2	PT0589	T-cell receptor be
130	10	37.0	6	2	PT0727	Ig heavy chain CRD
131	10	37.0	7	2	PT0246	aspartate transami
132	10	37.0	7	2	A11483	T-cell receptor be
133	10	37.0	7	2	PT0663	NADH2 dehydrogena
134	10	37.0	7	2	T09512	globulin IV alpha
135	10	37.0	7	2	S09066	T-cell receptor be
136	10	37.0	7	2	PT0529	trichodecentin I -
137	10	37.0	7	4	PC2056	protein Q430040 -
138	10	37.0	7	2	PC2057	polylactatase
139	10	37.0	8	2	PA0032	Ig gamma chain C r
140	10	37.0	8	2	S13661	T-cell receptor be
141	10	37.0	8	2	PT0627	T-cell receptor be
142	10	37.0	8	2	PT0522	T-cell receptor be
143	10	37.0	8	2	PT0559	T-cell receptor be
144	10	37.0	8	2	PT0554	T-cell receptor be
145	10	37.0	8	2	PT0725	R-phycocerythrin ga
146	10	37.0	8	2	A37521	sperm-activating p
147	10	37.0	8	2	F60588	sperm-activating p
148	10	37.0	8	2	E60588	sperm-activating p
149	10	37.0	8	2	G60588	sperm-activating p
150	10	37.0	8	2	G60588	sperm-activating p

ALIGNMENTS

RESULT 1
 A60654
 Substance P - guinea pig
 C/Species: Cavia porcellus (guinea pig)
 C/Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C/Accession: A60654
 R:Murphy, R.
 Neuropeptides 14, 105-110, 1989
 A/Title: Primary amino acid sequence of guinea-pig substance P.
 A/Reference number: A60654; MUID:90044685; PMID:2478925
 A/Accession: A60654
 A/Molecule type: protein
 A/Residues: 1-11 <MUR>
 A/Cross-references: UNIPROT:P01290
 C/Superfamily: substance P precursor
 C/Keywords: amidated carboxyl end; neuropeptide; tachykinin
 F/11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 27; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3;

Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	FFGLM 5							
Db	7	FFGLM 11							

RESULT 2
 SPHO
 Substance P - horse
 C/Species: Equus caballus (domestic horse)
 C/Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
 C/Accession: A01558
 R/Studer, R.O.; Tizzeck, A.; Lergier, W.
 Heiv. Chm. Acta 56, 860-866, 1973
 A/Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.
 A/Reference number: A01558
 A/Accession: A01558
 A/Molecule type: protein
 A/Residues: 1-11 <STU>
 A/Cross-references: UNIPROT:P01290
 C/Superfamily: substance P precursor
 C/Keywords: amidated carboxyl end; hormone
 F/11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 27; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	FFGLM 5
Db	7	FFGLM 11

RESULT 3
 JN0023
 Substance P - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C/Accession: JN0023
 R/Conlon, J.M.; Karsoulis, S.; Schmidt, W.E.; Thlm, L.
 Regul. Pept. 20, 171-180, 1988
 A/Title: [Arg3]substance P and neurokinin A from chicken small intestine.
 A/Reference number: JN0023; MUID:88204263; PMID:2452461
 A/Accession: JN0023
 A/Molecule type: protein
 A/Residues: 1-11 <CON>
 A/Cross-references: UNIPROT:P19850
 C/Superfamily: substance P precursor
 C/Keywords: amidated carboxyl end; tachykinin
 F/11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 27; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	FFGLM 5
Db	7	FFGLM 11

RESULT 4
 S33300
 Probable substance P - smaller spotted catshark
 C/Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S33300
 R/Waugh, D.; Wang, Y.; Hazon, N.; Balmont, R.J.; Conlon, J.M.
 Eur. J. Biochem. 214, 469-474, 1993
 A/Title: Primary structures and biological activities of substance-P-related peptides fr
 A/Reference number: S33300; MUID:93292508; PMID:7685693
 A/Accession: S33300
 A/Molecule type: protein

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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:13:37 / Search time 120.556 Seconds
(without alignments)
17.316 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-10-053-669-1
100.000

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 250346

Minimum DB seq length:

0

Maximum DB seq length:

11

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

1: /pub/pdb/1apb/1apb.pdb/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
7: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
9: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
13: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
18: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
19: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*
21: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*
22: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	5	9	US-09-265-690C-1
2	27	100.0	5	14	US-10-053-669-1
3	27	100.0	5	15	US-10-134-187-3
4	27	100.0	5	16	US-10-888-741-3
5	27	100.0	5	16	US-10-805-881-1
6	27	100.0	5	16	US-10-720-039-3
7	27	100.0	5	17	US-10-497-628-15
8	27	100.0	5	20	US-11-066-697-604
9	27	100.0	5	20	US-11-025-494-3
10	27	100.0	6	14	US-10-168-789A-38
11	27	100.0	6	17	US-10-497-628-14

12	27	100.0	6	20	US-11-066-697-595	Sequence 595, App
13	27	100.0	6	20	US-11-066-697-597	Sequence 597, App
14	27	100.0	6	20	US-11-066-697-601	Sequence 601, App
15	27	100.0	7	14	US-10-036-542-110	Sequence 110, App
16	27	100.0	7	14	US-10-036-542-111	Sequence 111, App
17	27	100.0	7	14	US-10-168-789A-37	Sequence 37, App
18	27	100.0	7	15	US-10-134-187-2	Sequence 2, App
19	27	100.0	7	16	US-10-688-741-2	Sequence 2, App
20	27	100.0	7	16	US-10-720-039-2	Sequence 2, App
21	27	100.0	7	17	US-10-497-628-13	Sequence 13, App
22	27	100.0	7	20	US-11-066-697-596	Sequence 596, App
23	27	100.0	7	20	US-11-066-697-607	Sequence 607, App
24	27	100.0	8	17	US-11-025-494-2	Sequence 2, App
25	27	100.0	8	14	US-10-168-789A-36	Sequence 36, App
26	27	100.0	8	17	US-10-497-628-12	Sequence 12, App
27	27	100.0	8	20	US-11-066-697-593	Sequence 593, App
28	27	100.0	8	20	US-11-066-697-592	Sequence 592, App
29	27	100.0	8	20	US-11-066-697-600	Sequence 600, App
30	27	100.0	9	14	US-10-036-542-112	Sequence 112, App
31	27	100.0	9	14	US-10-168-789A-35	Sequence 35, App
32	27	100.0	9	15	US-10-134-187-1	Sequence 1, App
33	27	100.0	9	16	US-10-688-741-1	Sequence 1, App
34	27	100.0	9	16	US-10-720-039-1	Sequence 1, App
35	27	100.0	9	20	US-11-066-697-545	Sequence 545, App
36	27	100.0	9	20	US-11-066-697-622	Sequence 622, App
37	27	100.0	9	20	US-11-025-494-1	Sequence 1, App
38	27	100.0	10	14	US-10-168-789A-34	Sequence 34, App
39	27	100.0	10	14	US-10-451-304-1	Sequence 1, App
40	27	100.0	10	20	US-11-066-697-621	Sequence 621, App
41	27	100.0	10	20	US-11-079-147-71	Sequence 71, App
42	27	100.0	11	9	US-09-935-690C-3	Sequence 3, App
43	27	100.0	11	9	US-09-935-690C-4	Sequence 4, App
44	27	100.0	11	9	US-09-841-091B-26	Sequence 26, App
45	27	100.0	11	10	US-09-988-792-1	Sequence 1, App
46	27	100.0	11	10	US-09-988-792-6	Sequence 6, App
47	27	100.0	11	10	US-09-988-792-7	Sequence 7, App
48	27	100.0	11	10	US-09-988-792-8	Sequence 8, App
49	27	100.0	11	10	US-09-988-792-10	Sequence 10, App
50	27	100.0	11	13	US-10-002-593-4	Sequence 4, App
51	27	100.0	11	14	US-10-230-133-1	Sequence 1, App
52	27	100.0	11	14	US-10-053-669-3	Sequence 3, App
53	27	100.0	11	14	US-10-211-994-3	Sequence 3, App
54	27	100.0	11	14	US-10-114-828B-24	Sequence 24, App
55	27	100.0	11	14	US-10-197-954-130	Sequence 130, App
56	27	100.0	11	14	US-10-251-703-25	Sequence 25, App
57	27	100.0	11	14	US-10-168-789A-17	Sequence 17, App
58	27	100.0	11	14	US-10-423-714-4	Sequence 4, App
59	27	100.0	11	15	US-10-343-654-27	Sequence 27, App
60	27	100.0	11	15	US-10-289-009-24	Sequence 24, App
61	27	100.0	11	15	US-10-289-009-25	Sequence 25, App
62	27	100.0	11	15	US-10-289-009-26	Sequence 26, App
63	27	100.0	11	15	US-10-167-627-65	Sequence 65, App
64	27	100.0	11	16	US-10-695-536-1	Sequence 1, App
65	27	100.0	11	16	US-10-805-881-3	Sequence 3, App
66	27	100.0	11	16	US-10-813-856-4	Sequence 4, App
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ALIGNMENTS

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; Publication No. US20010051345A1
; GENERAL INFORMATION:
; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265, 690C
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
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US-09-265-690C-1
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Best Local Similarity 100.0%; Pred.No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: N1427-005
; CURRENT APPLICATION NUMBER: US/10/053, 669
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 09/265, 690
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
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; TYPE: PRT
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Db      1  FFGLM 5
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; Publication No. US20030202981A1
; GENERAL INFORMATION:
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; TITLE OF INVENTION: Chimeric Hybrid Analgesics
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ALIGNMENTS

RESULT 1
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Sequence 2, Application US/07934553
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GENERAL INFORMATION:
APPLICANT: PATTERSON, ROY
APPLICANT: HARRIS, KATHLEEN E
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: TILTON, FALLON, LUNGUMUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,553
FILING DATE: 19920821
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: FENTRESS, SUSAN B
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9033CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/456-8000
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-934-553-2

Query Match 100.0%; Score 27; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PFGLM 5
Db 1 PFGLM 5

RESULT 2
US-08-225-474-2
Sequence 2, Application US/08225474
Patent No. 5560915
GENERAL INFORMATION:
APPLICANT: Patterson, Roy
APPLICANT: Harris, Kathleen E
TITLE OF INVENTION: Method and Composition for Treating
TITLE OF INVENTION: Ige Mediated Allergies
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
STREET: 100 S. Wacker Drive, Suite 960
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,474
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,553
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.
REGISTRATION NUMBER: 16,926
REFERENCE/DOCKET NUMBER: NU 9033-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)-456-8000

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:08:06 ; Search time 133.333 Seconds
(without alignments)
14.504 Million cell updates/sec

Title: GUS100506699=1
Perfect score: 27
Sequence: 1 FGLM 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 494136

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 150 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	5	2 AAR33009	Aar33009 Alpha-sub
2	27	100.0	5	2 AAR33008	Aar33008 Alpha-sub
3	27	100.0	5	2 AAR33007	Aar33007 Alpha-sub
4	27	100.0	5	2 AAR33010	Aar33010 Alpha-sub
5	27	100.0	5	2 AAR54549	Aar54549 Cholecyt
6	27	100.0	5	2 AAR54551	Aar54551 Cholecyt
7	27	100.0	5	2 AAR54550	Aar54550 Cholecyt
8	27	100.0	5	2 AAR54548	Aar54548 Cholecyt
9	27	100.0	5	2 AAR41687	Aar41687 Tetrapept
10	27	100.0	5	2 AAR99643	Aar99643 Substance
11	27	100.0	5	2 AAY50325	Aay50325 Neutrophil
12	27	100.0	5	2 AAM92660	Aam92660 Human tac
13	27	100.0	5	3 AAB23025	Aab23025 Human/rat
14	27	100.0	5	3 AAY67576	Aay67576 P antagonist
15	27	100.0	5	4 AAB91428	Aab91428 Tachykini
16	27	100.0	5	5 AAB10088	Abb10088 Substance
17	27	100.0	5	5 AAU77845	Aau77845 Tachykini
18	27	100.0	5	7 ADE94203	Ade94203 High acti
19	27	100.0	5	8 ADF92530	Adf92530 Mammalian
20	27	100.0	5	8 ADN95078	Adn95078 Human mag
21	27	100.0	6	1 AAR43771	Aar43771 Human mag
22	27	100.0	6	1 AAP40519	Aap40519 Sequence
23	27	100.0	6	1 AAP50694	Aap50694 Substance
24	27	100.0	6	1 AAP50632	Aap50632 Substance
25	27	100.0	6	1 AAP61486	Aap61486 Peptide h

26	27	100.0	6	2 AAR07893	Aar07893 Cyllopept
27	27	100.0	6	2 AAR21959	Aar21959 Substance
28	27	100.0	6	2 AAR27694	Aar27694 Cyclic ta
29	27	100.0	6	2 AAW9686	Aaw9686 Substance
30	27	100.0	6	2 AAR92706	Aar92706 Human tac
31	27	100.0	6	2 AAW92659	Aaw92659 Human tac
32	27	100.0	6	3 AAY67575	Aay67575 P antagonist
33	27	100.0	6	4 AAB82453	Aab82453 Fluorinat
34	27	100.0	6	4 AAB82436	Aab82436 Fluorinat
35	27	100.0	6	4 AAB91421	Aab91421 Tachykini
36	27	100.0	6	4 AAB91425	Aab91425 Tachykini
37	27	100.0	6	4 AAB91419	Aab91419 Tachykini
38	27	100.0	6	4 AAG99351	Aag99351 Acypical
39	27	100.0	6	4 AAB98884	Aab98884 Chimeric
40	27	100.0	6	4 AAB98886	Aab98886 Chimeric
41	27	100.0	6	5 AAB10086	Abb10086 Substance
42	27	100.0	6	7 ADB94202	Adb94202 High acti
43	27	100.0	7	2 AAR21956	Aar21956 Substance
44	27	100.0	7	2 AAR21957	Aar21957 Substance
45	27	100.0	7	2 AAY50324	Aay50324 Neutrophil
46	27	100.0	7	2 AAW92662	Aaw92662 Human tac
47	27	100.0	7	2 AAW92705	Aaw92705 Human tac
48	27	100.0	7	3 AAY67574	Aay67574 P antagonist
49	27	100.0	7	4 AAB80323	Aab80323 Human pro
50	27	100.0	7	4 AAB80324	Aab80324 Human pro
51	27	100.0	7	4 AAB91431	Aab91431 Tachykini
52	27	100.0	7	4 AAB91420	Aab91420 Tachykini
53	27	100.0	7	4 AAG99350	Aag99350 Acypical
54	27	100.0	7	4 AAB98845	Aab98845 Chimeric
55	27	100.0	7	5 AAB09500	Abb09500 Substance
56	27	100.0	7	7 ADB94201	Adb94201 High acti
57	27	100.0	7	7 ADF92529	Adf92529 Substance
58	27	100.0	7	8 ADN95077	Adn95077 Mammalian
59	27	100.0	8	1 AAP20303	Aap20303 Gastroint
60	27	100.0	8	2 AAR28444	Aar28444 Neutrophil
61	27	100.0	8	2 AAW92664	Aaw92664 Human tac
62	27	100.0	8	2 AAW92710	Aaw92710 Human tac
63	27	100.0	8	3 AAY67573	Aay67573 P antagonist
64	27	100.0	8	4 AAB91407	Aab91407 Tachykini
65	27	100.0	8	4 AAB91416	Aab91416 Tachykini
66	27	100.0	8	4 AAB91424	Aab91424 Tachykini
67	27	100.0	8	4 AAG99349	Aag99349 Acypical
68	27	100.0	8	5 ABB09498	Abb09498 Substance
69	27	100.0	8	7 ADB94200	Adb94200 High acti
70	27	100.0	9	1 AAP50634	Aap50634 Substance
71	27	100.0	9	2 AAR92714	Aar92714 Human tac
72	27	100.0	9	4 AAB80325	Aab80325 Human pro
73	27	100.0	9	4 AAB91446	Aab91446 Tachykini
74	27	100.0	9	4 AAB91369	Aab91369 Tachykini
75	27	100.0	9	4 AAG99348	Aag99348 Acypical
76	27	100.0	9	7 ADF92528	Adf92528 Substance
77	27	100.0	9	8 ADN95076	Adn95076 Mammalian
78	27	100.0	10	1 AAP50633	Aap50633 Substance
79	27	100.0	10	2 AAR21933	Aar21933 Substance
80	27	100.0	10	2 AAR65181	Aar65181 S. cerevi
81	27	100.0	10	2 AAY06939	Aay06939 Substance
82	27	100.0	10	2 AAW92663	Aaw92663 Human tac
83	27	100.0	10	4 AAB91445	Aab91445 Tachykini
84	27	100.0	10	4 AAG99347	Aag99347 Acypical
85	27	100.0	10	4 AAG64746	Aag64746 Substance
86	27	100.0	10	8 ADN12181	Adn12181 Amino aci
87	27	100.0	10	8 ADN27868	Adn27868 Trichomon
88	27	100.0	11	1 AAP61480	Aap61480 Sequence
89	27	100.0	11	1 AAP80312	Aap80312 Sequence
90	27	100.0	11	2 AAR11854	Aar11854 Undecapep
91	27	100.0	11	2 AAR13162	Aar13162 Sialic ac
92	27	100.0	11	2 AAR28442	Aar28442 Substance
93	27	100.0	11	2 AAR21942	Aar21942 Substance
94	27	100.0	11	2 AAR21962	Aar21962 Substance
95	27	100.0	11	2 AAR21945	Aar21945 Substance
96	27	100.0	11	2 AAR21963	Aar21963 Substance
97	27	100.0	11	2 AAR21949	Aar21949 Substance
98	27	100.0	11	2 AAR21951	Aar21951 Substance

99	27	100.0	11	2	AAR21946	Aar21946	Substance
100	27	100.0	11	2	AAR21964	Aar21964	Substance
101	27	100.0	11	2	AAR21970	Aar21970	Cyclic su
102	27	100.0	11	2	AAR21938	Aar21938	Substance
103	27	100.0	11	2	AAR21941	Aar21941	Substance
104	27	100.0	11	2	AAR21954	Aar21954	Substance
105	27	100.0	11	2	AAR42646	Aar42646	Substance
106	27	100.0	11	2	AAR85243	Aar85243	Substance
107	27	100.0	11	2	AAR77310	Aar77310	Substance
108	27	100.0	11	2	AAW3181	AAW3181	Mono-DTPA
109	27	100.0	11	2	AAW3180	AAW3180	Mono-DTPA
110	27	100.0	11	2	AAW4616	AAW4616	Substance
111	27	100.0	11	2	AAW79775	AAW79775	Substance
112	27	100.0	11	2	AAW42973	AAW42973	Substrate
113	27	100.0	11	2	AAW79663	AAW79663	Substance
114	27	100.0	11	2	AAW79662	AAW79662	Substance
115	27	100.0	11	2	AAW92679	AAW92679	Human tac
116	27	100.0	11	2	AAW92675	AAW92675	Human tac
117	27	100.0	11	2	AAW92720	AAW92720	Human tac
118	27	100.0	11	2	AAW92673	AAW92673	Human tac
119	27	100.0	11	2	AAW92708	AAW92708	Human tac
120	27	100.0	11	2	AAW92731	AAW92731	Human tac
121	27	100.0	11	2	AAW92670	AAW92670	Human tac
122	27	100.0	11	2	AAW92689	AAW92689	Human tac
123	27	100.0	11	2	AAW92715	AAW92715	Human tac
124	27	100.0	11	2	AAW92719	AAW92719	Human tac
125	27	100.0	11	2	AAW92680	AAW92680	Human tac
126	27	100.0	11	2	AAW92681	AAW92681	Human tac
127	27	100.0	11	2	AAW92672	AAW92672	Human tac
128	27	100.0	11	2	AAW92690	AAW92690	Human tac
129	27	100.0	11	2	AAW30985	AAW30985	Non-cross
130	27	100.0	11	2	AAW03156	AAW03156	Substance
131	27	100.0	11	2	AD124903	AD124903	Substance
132	27	100.0	11	3	AAB23027	Aab23027	Human/rat
133	27	100.0	11	3	AAB18483	Aab18483	Cell diff
134	27	100.0	11	3	AAV32382	Aav32382	Peptide s
135	27	100.0	11	3	AAB06260	Aab06260	Substance
136	27	100.0	11	3	AAB08614	Aab08614	Peptide 1
137	27	100.0	11	4	AAB50311	Aab50311	Prevln pe
138	27	100.0	11	4	AAB50312	Aab50312	Prevln pe
139	27	100.0	11	4	AAB50306	Aab50306	Substance
140	27	100.0	11	4	AAB50316	Aab50316	Prevln pe
141	27	100.0	11	4	AAB50544	Aab50544	Prolyl en
142	27	100.0	11	4	AAB91450	Aab91450	Tachykini
143	27	100.0	11	4	AAB91438	Aab91438	Tachykini
144	27	100.0	11	4	AAB91449	Aab91449	Tachykini
145	27	100.0	11	4	AAB91402	Aab91402	Tachykini
146	27	100.0	11	4	AAB91436	Aab91436	Tachykini
147	27	100.0	11	4	AAG93358	Aag93358	ATT-short
148	27	100.0	11	4	AAG93354	Aag93354	Substance
149	27	100.0	11	4	AAG93337	Aag93337	Human aty
150	27	100.0	11	4	AAU07298	Aau07298	Substance

ALIGNMENTS

RESULT 1

AAR33009
ID AAR33009 standard; peptide; 5 AA.

AC AAR33009;

DT 25-MAR-2003 (revised)

DT 02-APR-1993 (first entry)

XX Alpha-substituted short peptide.

XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;

XX improved bioavailability.

XX Synthetic.

XX

PH	Key	Location/Qualifiers
FT	Modified-site	4
FT	Modified-site	/note= "alpha-Me-Leu"
FT	Modified-site	5
FT	Modified-site	/note= "Met-NH2"
XX		
XX	WO9219254-A1.	
XX		
XX	12-NOV-1992.	
XX		
XX	15-APR-1992;	92WO-US003119.
XX		
XX	24-APR-1991;	91US-00690755.
XX	20-MAR-1992;	92US-00852086.
XX	(WARN) WARNER LAMBERT CO.	
PI	Horwell DC, Hughes J, Richardson RS, Howson W,	
XX	WPI; 1992-398522/48.	
XX		
PT	New alpha-substd. polypeptide are e.g. selective receptor ligands - for	
PT	treating inflammation, pain, stroke, ulcers, hypertension, heart failure,	
PT	depression, cancer, asthma, psychosis, arthritis, etc.	
XX		
XX	Claim 3; Page 41; 46pp; English.	
PS		
CC	The peptide is a specifically claimed example of a group of generically	
CC	claimed mono-, di-, tri-, tetra- and penta-peptides which include a	
CC	substituent on an alpha-C atom in the chain. Such substitution may modify	
CC	the bioavailability, stability or absorbability of the peptide and hence	
CC	may improve the activity of the peptide as a drug. Depending on the	
CC	nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic	
CC	peptide, etc.), the modified peptides are variously useful for treating	
CC	obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,	
CC	addictive drug withdrawal symptoms, hypertension, heart failure,	
CC	cognition or memory disorders, spasticity, depression, diabetes, cancer,	
CC	asthma, bladder dysfunction, psychosis and arthritis; and as	
CC	contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on	
CC	25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR	
CC	field.) (Updated on 25-MAR-2003 to correct PI field.)	
XX		
SQ	Sequence 5 AA;	
	Query Match	100.0%; Score 27; DB 2; Length 5;
	Best Local Similarity	100.0%; Pred. No. 1.8e+06;
	Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 FFGLM 5	
DB	1 FFGLM 5	

RESULT 2

AAR33008
ID AAR33008 standard; peptide; 5 AA.

AC AAR33008;

DT 25-MAR-2003 (revised)

DT 02-APR-1993 (first entry)

XX Alpha-substituted short peptide.

XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;

XX improved bioavailability.

XX Synthetic.

XX Key

XX Modified-site

XX Modified-site

XX Modified-site

XX Modified-site

XX Modified-site

XX Modified-site

XX Modified-site

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OM protein - protein search, using SW model

Run on: October 26, 2005, 08:01:20 ; Search time 102.222 Seconds
(without alignments)
20.038 Million cell updates/sec

Title: us-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB-seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : uniprot_03_*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	11	1	TKN4_PSEBU
2	21	100.0	11	1	TKN5_PSEBU
3	21	100.0	11	1	TKNA_CAVBO
4	21	100.0	11	1	TKNA_CHICK
5	21	100.0	11	1	TKNA_HORSE
6	21	100.0	11	1	TKNA_ONCMY
7	21	100.0	11	1	TKNA_SCVCA
8	21	100.0	19	2	PA2S_HUMAN
9	21	100.0	19	2	Q9SBE2
10	21	100.0	41	2	Q7UPW5
11	21	100.0	45	2	Q6LD93
12	21	100.0	46	2	Q87RM6
13	21	100.0	53	2	Q9TY14
14	21	100.0	55	2	Q17544
15	21	100.0	55	2	Q4360
16	21	100.0	56	1	VRZK_BACSU
17	21	100.0	58	2	Q8EMW4
18	21	100.0	63	2	Q6R1A0
19	21	100.0	63	2	Q9GML1
20	21	100.0	63	2	Q6ZBO3
21	21	100.0	63	2	Q82X04
22	21	100.0	64	2	Q86H30
23	21	100.0	67	2	Q8TLV1
24	21	100.0	67	2	Q8GTG4
25	21	100.0	68	2	Q05625
26	21	100.0	68	2	Q05886
27	21	100.0	69	1	Y010_TROW8
28	21	100.0	69	1	Y010_TROW8
29	21	100.0	69	1	YAT1_RHOBL
30	21	100.0	72	2	Q9Y494
31	21	100.0	72	2	Q9GP92

32	21	100.0	72	2	Q8CSF7	Q8CSF7 staphylococ
33	21	100.0	74	2	Q8IWZ7	Q8IWZ7 homo sapien
34	21	100.0	76	2	Q86UW6	Q86UW6 homo sapien
35	21	100.0	78	2	Q8VW82	Q8VW82 colwellia m
36	21	100.0	78	2	Q8UKO3	Q8UKO3 agrobacteri
37	21	100.0	79	2	Q8HN49	Q8HN49 brugia mala
38	21	100.0	79	2	Q8K214	Q8K214 uncultured
39	21	100.0	80	2	Q47577	Q47577 onchocerca
40	21	100.0	80	2	Q98N11	Q98N11 rhizobium 1
41	21	100.0	81	2	Q8XN79	Q8XN79 clostridium
42	21	100.0	81	2	Q7MD50	Q7MD50 vibrio vuln
43	21	100.0	81	2	Q8D627	Q8D627 vibrio vuln
44	21	100.0	82	2	Q6ECK5	Q6ECK5 oryctolagus
45	21	100.0	83	2	Q6TRW3	Q6TRW3 sulfolobus
46	21	100.0	84	2	Q6TWP5	Q6TWP5 aryaia de
47	21	100.0	84	2	Q6YMP7	Q6YMP7 aryaia de
48	21	100.0	84	2	Q8B405	Q8B405 streptococ
49	21	100.0	84	2	Q99927	Q99927 carnation m
50	21	100.0	84	2	Q683S5	Q683S5 carnation m
51	21	100.0	85	2	Q26173	Q26173 methanobact
52	21	100.0	87	2	Q86UW7	Q86UW7 homo sapien
53	21	100.0	88	2	Q8L778	Q8L778 vibriophag
54	21	100.0	88	2	Q7UCH0	Q7UCH0 rhodospirill
55	21	100.0	89	2	Q49761	Q49761 mycobacteri
56	21	100.0	90	1	Y040_CORGL	Y040_CORGL
57	21	100.0	90	1	YF1M_ECOLI	YF1M_ECOLI
58	21	100.0	90	2	Q8H9X0	Q8H9X0 pseudomonas
59	21	100.0	90	2	Q94JMG	Q94JMG oryza sativ
60	21	100.0	90	2	Q7UBW7	Q7UBW7 shigella fl
61	21	100.0	90	2	Q8X9F4	Q8X9F4 escherichia
62	21	100.0	93	2	Q658H4	Q658H4 oryza sativ
63	21	100.0	93	2	Q92916	Q92916 escherichia
64	21	100.0	95	1	MG8B_HUMAN	MG8B_HUMAN
65	21	100.0	96	1	Y87A_HAEIN	Y87A_HAEIN
66	21	100.0	96	2	Q6MOE2	Q6MOE2 methanococ
67	21	100.0	96	2	Q86U08	Q86U08 homo sapien
68	21	100.0	97	2	Q68974	Q68974 synechococ
69	21	100.0	97	2	Q920K2	Q920K2 cavia porce
70	21	100.0	99	2	Q9RD07	Q9RD07 streptomyce
71	21	100.0	100	2	Q6ECK6	Q6ECK6 cryotolagus
72	21	100.0	100	2	Q63W33	Q63W33 burkholderi
73	21	100.0	102	2	Q9YG57	Q9YG57 aeropyrum p
74	21	100.0	104	2	Q6SGW8	Q6SGW8 uncultured
75	21	100.0	104	2	Q92MW6	Q92MW6 rhizobium m
76	21	100.0	104	2	Q7VC12	Q7VC12 prochloroxo
77	21	100.0	105	2	Q9YCF6	Q9YCF6 aeropyrum p
78	21	100.0	106	2	Q9PMK7	Q9PMK7 campylobact
79	21	100.0	107	2	Q6ECK8	Q6ECK8 homo sapien
80	21	100.0	107	2	Q7X2C5	Q7X2C5 rhodocyclus
81	21	100.0	107	2	Q6NBV3	Q6NBV3 rhodopseudo
82	21	100.0	107	2	Q8E527	Q8E527 streptococ
83	21	100.0	108	2	Q8FWT0	Q8FWT0 brucella su
84	21	100.0	109	2	Q16164	Q16164 homo sapien
85	21	100.0	109	2	Q9G049	Q9G049 phage phi11h
86	21	100.0	109	2	Q8H7P1	Q8H7P1 oryza sativ
87	21	100.0	109	2	Q6SK09	Q6SK09 bacillus th
88	21	100.0	109	2	Q81X85	Q81X85 bacillus an
89	21	100.0	110	1	COX4_BACSU	COX4_BACSU
90	21	100.0	111	2	Q6M195	Q6M195 methanococ
91	21	100.0	112	2	Q9XES4	Q9XES4 arabidopsis
92	21	100.0	113	2	Q86UT9	Q86UT9 homo sapien
93	21	100.0	113	2	Q7NHZ1	Q7NHZ1 gloeobacter
94	21	100.0	114	1	YE96_METUA	YE96_METUA
95	21	100.0	114	2	Q97947	Q97947 cupaia glis
96	21	100.0	114	2	Q83K17	Q83K17 shigella fl
97	21	100.0	114	2	Q8FP03	Q8FP03 escherichia
98	21	100.0	115	1	TKN1_RABIT	TKN1_RABIT
99	21	100.0	115	2	Q6M4R0	Q6M4R0 oryctolagus
100	21	100.0	115	2	Q920K1	Q920K1 vibrio angu
101	21	100.0	116	2	Q6YU06	Q6YU06 cavia porce
102	21	100.0	116	2	Q9HXG9	Q9HXG9 pseudomonas
103	21	100.0	116	2	Q9X1V2	Q9X1V2 thermotoga
104	21	100.0	117	1	NU3W_BRALA	NU3W_BRALA

ID	TKN4_PSECU	STANDARD;	PRT;	11 AA.
105	21	100.0	117	2
106	21	100.0	117	2
107	21	100.0	117	2
108	21	100.0	118	2
109	21	100.0	119	2
110	21	100.0	121	2
111	21	100.0	123	2
112	21	100.0	124	2
113	21	100.0	124	2
114	21	100.0	125	2
115	21	100.0	125	2
116	21	100.0	125	2
117	21	100.0	126	2
118	21	100.0	128	2
119	21	100.0	128	2
120	21	100.0	128	2
121	21	100.0	129	1
122	21	100.0	129	1
123	21	100.0	129	2
124	21	100.0	130	2
125	21	100.0	130	1
126	21	100.0	130	1
127	21	100.0	130	1
128	21	100.0	130	1
129	21	100.0	131	1
130	21	100.0	131	2
131	21	100.0	131	2
132	21	100.0	132	1
133	21	100.0	132	2
134	21	100.0	132	2
135	21	100.0	133	2
136	21	100.0	133	2
137	21	100.0	133	2
138	21	100.0	134	2
139	21	100.0	134	1
140	21	100.0	134	1
141	21	100.0	134	2
142	21	100.0	134	2
143	21	100.0	134	2
144	21	100.0	134	2
145	21	100.0	136	1
146	21	100.0	136	2
147	21	100.0	137	1
148	21	100.0	137	2
149	21	100.0	137	2
150	21	100.0	137	2

ALIGNMENTS

RESULT 1
TKN4_PSECU
ID TKN4_PSECU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Substance P-like peptide I (PG-SP1).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_Taxid=30349;
RN [1]
RP SEQUENCE
RC TISSUE=Skin secretion;
RC MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;
RA Simmaco M., Severini C., de Biase D., Barra D., Bosca F.,
RA Roberts J.D., Melchiorri P., Ersamer V.,
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.",
RP Peptides 11:299-304(1990).

CC - FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: Skin.
CC - SIMILARITY: Belongs to the tachykinin family.
DR PIR; E60409; E60409.
DR InterPro; IPR002040; Tachy Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing;
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
FT MOD RES 1 1
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1A87 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FGLM 4
DB 8 FGLM 11

RESULT 2
TKN5_PSECU
ID TKN5_PSECU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Substance P-like peptide II (PG-SP11).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_Taxid=30349;
RN [1]
RP SEQUENCE
RC TISSUE=Skin secretion;
RC MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;
RA Simmaco M., Severini C., de Biase D., Barra D., Bosca F.,
RA Roberts J.D., Melchiorri P., Ersamer V.,
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.",
RL Peptides 11:299-304(1990).
CC - FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: Skin.
CC - SIMILARITY: Belongs to the tachykinin family.
DR PIR; F60409; F60409.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing;
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
FT MOD RES 1 1
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1A57 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FGLM 4
DB 8 FGLM 11

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 26, 2005, 08:04:16 ; Search time 10.6667 Seconds
(without alignments)
36.081 Million cell updates/sec

Title: US-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : PIR 79:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	11	1 A60654	substance P - guin
2	21	100.0	11	1 SPHO	substance P - hoxa
3	21	100.0	11	2 JN0023	substance P - chic
4	21	100.0	11	2 S33300	probable substance
5	21	100.0	11	2 E60409	substance P-like P
6	21	100.0	11	2 E60409	substance P-like P
7	21	100.0	11	2 S23308	substance P - rain
8	21	100.0	19	2 PS0332	phospholipase A2 (
9	21	100.0	56	2 A69983	hypothetical prote
10	21	100.0	63	2 JC2412	tachykinin gamma c
11	21	100.0	69	2 S04666	hypothetical prote
12	21	100.0	72	2 JC5455	preprotachykinin-A
13	21	100.0	72	2 T23860	tachykinin A gamma
14	21	100.0	72	2 T23860	hypothetical prote
15	21	100.0	78	2 AE3165	hypothetical prote
16	21	100.0	80	2 T11069	NMDH2 dehydrogenas
17	21	100.0	85	2 H69191	hypothetical prote
18	21	100.0	89	2 S72598	sulfate permease T
19	21	100.0	90	2 C85905	hypothetical prote
20	21	100.0	90	2 E91060	hypothetical prote
21	21	100.0	97	2 A65037	hypothetical prote
22	21	100.0	97	2 S12958	tachykinin delta P
23	21	100.0	102	2 G72756	hypothetical prote
24	21	100.0	105	2 F72614	hypothetical prote
25	21	100.0	106	2 G81275	hypothetical prote
26	21	100.0	109	2 I52333	G1 phase-specific
27	21	100.0	110	2 G69609	cytochrome-c oxida
28	21	100.0	112	1 SPRTA	substance P alpha
29	21	100.0	112	2 T51238	searcrow-like pro

30	21	100.0	115	1 SPRBG	substance P gamma
31	21	100.0	115	2 S47039	tachykinin 1 precu
32	21	100.0	116	2 H83167	hypothetical prote
33	21	100.0	116	2 C72232	hypothetical prote
34	21	100.0	117	2 A71391	NMDH2 dehydrogenas
35	21	100.0	117	2 G64486	hypothetical prote
36	21	100.0	117	2 B86771	hypothetical prote
37	21	100.0	114	2 E97098	Zn-finger contain
38	21	100.0	126	2 S70624	cytochrome P450 CY
39	21	100.0	128	2 A88072	protein ZK1240.6 [
40	21	100.0	129	1 SPHRB	neurokinin 1 precu
41	21	100.0	129	2 A82227	conserved hypochet
42	21	100.0	130	1 SPBOB	neurokinin 1 precu
43	21	100.0	130	1 SPRTB	substance P beta P
44	21	100.0	130	2 S47038	tachykinin 1 precu
45	21	100.0	130	2 T52526	neurokinin 1 precu
46	21	100.0	131	2 AG0070	conserved hypochet
47	21	100.0	132	2 AD0895	probable membrane
48	21	100.0	133	2 C24925	lactose permease -
49	21	100.0	133	2 G69137	DNA-dependent RNA
50	21	100.0	134	2 H65098	hypothetical prote
51	21	100.0	134	2 D85971	hypothetical prote
52	21	100.0	134	2 E91126	hypothetical prote
53	21	100.0	134	2 T43561	probable transpos
54	21	100.0	136	2 S04226	hemoglobin II - C1
55	21	100.0	137	1 R5YM16	ribosomal protein
56	21	100.0	138	2 G82915	ribosomal protein
57	21	100.0	145	2 H70346	hypothetical prote
58	21	100.0	147	2 AC1223	ethanolamine util
59	21	100.0	148	2 AF1576	ethanolamine util
60	21	100.0	152	2 T03456	cobd protein - Rho
61	21	100.0	152	2 B72317	hypothetical prote
62	21	100.0	155	2 B83004	hypothetical prote
63	21	100.0	160	2 G83300	hypothetical prote
64	21	100.0	163	2 T36985	hypothetical prote
65	21	100.0	166	2 AG1931	hypothetical prote
66	21	100.0	167	2 T11465	NMDH2 dehydrogenas
67	21	100.0	168	2 T03141	hypothetical prote
68	21	100.0	169	2 P00185	conoplaet incirnal
69	21	100.0	169	2 E87657	hypothetical prote
70	21	100.0	172	2 T20329	hypothetical prote
71	21	100.0	173	2 E83931	hypothetical prote
72	21	100.0	174	2 E82122	purine-binding che
73	21	100.0	176	2 T45308	hypothetical prote
74	21	100.0	177	2 T01346	hypothetical prote
75	21	100.0	177	2 T45675	hypothetical prote
76	21	100.0	180	2 S77046	hypothetical prote
77	21	100.0	185	1 A59351	lysosyme (EC 3.2.1
78	21	100.0	185	1 LZGSG	lysosyme (EC 3.2.1
79	21	100.0	185	1 LZGSG	lysosyme (EC 3.2.1
80	21	100.0	185	1 LZMGS	lysosyme (EC 3.2.1
81	21	100.0	185	2 JC7955	lysosyme (EC 3.2.1
82	21	100.0	185	2 A59488	lysosyme g - Chine
83	21	100.0	185	2 A96615	probable dirigent
84	21	100.0	189	2 F82969	hypothetical prote
85	21	100.0	194	2 G71698	lipoprotein signal
86	21	100.0	196	2 S45553	spor maturation p
87	21	100.0	200	2 B71879	hypothetical prote
88	21	100.0	200	2 E64636	hypothetical prote
89	21	100.0	206	2 S56133	dicarboxylate tran
90	21	100.0	206	2 F97769	signal peptidase I
91	21	100.0	207	2 F69609	cytochrome-c oxida
92	21	100.0	209	1 C69796	conserved hypochet
93	21	100.0	210	2 F64115	hypothetical prote
94	21	100.0	210	2 T40465	probable mitosis a
95	21	100.0	211	2 S18463	lysosyme (EC 3.2.1
96	21	100.0	213	2 G72276	phosphoribosylform
97	21	100.0	214	2 AG2684	RhtB family transp
98	21	100.0	215	2 AD0681	probable ABC trans
99	21	100.0	215	2 T22446	hypothetical prote
100	21	100.0	216	2 AH0120	probable membrane
101	21	100.0	217	2 F83840	stage II sporulati
102	21	100.0	220	2 A95362	Probable inner-mem

103	21	100.0	221	2	A10360	conserved hypochet
104	21	100.0	223	2	C81397	phosphoribosylform
105	21	100.0	223	2	H81219	NADH dehydrogenase
106	21	100.0	223	2	H81991	NADH dehydrogenase
107	21	100.0	224	2	C69687	menaquinol-cytochr
108	21	100.0	224	2	B29503	hypothetical prote
109	21	100.0	224	2	E97466	hypothetical prote
110	21	100.0	228	2	E86849	glutamate ABC tran
111	21	100.0	228	2	AD1024	conserved hypochet
112	21	100.0	229	2	H97147	enoyl-CoA hydratase
113	21	100.0	230	1	H64634	conserved hypochet
114	21	100.0	230	2	F71879	hypothetical prote
115	21	100.0	231	2	A75462	conserved hypochet
116	21	100.0	231	2	H75465	hypothetical prote
117	21	100.0	232	1	B70167	conserved hypochet
118	21	100.0	232	2	JC5010	nucleotide-binding
119	21	100.0	232	2	H69294	conserved hypochet
120	21	100.0	233	2	C71848	purine nucleoside
121	21	100.0	233	2	AH1218	Salmonella typhimu
122	21	100.0	234	2	F75254	conserved hypochet
123	21	100.0	235	2	G69882	hypothetical prote
124	21	100.0	235	2	F71249	hypothetical prote
125	21	100.0	236	2	A75455	hypothetical prote
126	21	100.0	237	1	S76661	hypothetical prote
127	21	100.0	239	2	S40143	nitrate transporte
128	21	100.0	239	2	AE0772	probable exported
129	21	100.0	240	2	H70091	hypothetical prote
130	21	100.0	242	1	F64123	dethiobiotin synth
131	21	100.0	242	2	JC5883	myocyte enhancer f
132	21	100.0	243	2	AG2395	hypothetical prote
133	21	100.0	245	2	E81023	ABC transporter, A
134	21	100.0	245	2	E81968	probable ABC trans
135	21	100.0	246	2	H84127	enoyl CoA hydratase
136	21	100.0	247	2	H69493	phosphoserine-re
137	21	100.0	247	2	E82555	heme ABC transport
138	21	100.0	248	2	F75200	hypothetical prote
139	21	100.0	249	2	A71234	hypothetical prote
140	21	100.0	251	2	B84016	hypothetical prote
141	21	100.0	253	2	C82517	conserved hypochet
142	21	100.0	255	2	G75157	abc transporter, A
143	21	100.0	256	2	J01106	tonoplast intrinsi
144	21	100.0	256	2	S26742	tonoplast intrinsi
145	21	100.0	256	2	D81181	conserved hypochet
146	21	100.0	256	2	C81925	probable sec-indep
147	21	100.0	259	2	B83838	oxidoreductase BHI
148	21	100.0	259	2	D83216	probable aldolase
149	21	100.0	261	2	C86207	hypothetical prote
150	21	100.0	265	2	G70888	hypothetical prote

ALIGNMENTS

RESULT 1
 A60654
 Substance P - guinea pig
 C:Species: Cavia porcellus (guinea pig)
 C>Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C/Accession: A60654

R/Murphy, R.
 Neuropeptides 14, 105-110, 1989
 A>Title: Primary amino acid sequence of guinea-pig substance P.
 A/Reference number: A60654; MUID:90044685; PMID:2478925

A/Accession: A60654
 A/Molecule type: protein

A/Residues: 1-11 <MUR>
 A/Cross-references: UNIPROT:P01290

C/Superfamily: Substance P precursor
 C/Keywords: amidated carboxyl end; neuropeptide; tachykinin

F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 21; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 19;

Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	FGIM	4						
Db	8	FGIM	11						

RESULT 2

SPHO
 Substance P - horse

C:Species: Equus caballus (domestic horse)

C>Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C/Accession: A01558

R/Studer, R.O.; Trzeciak, A.; Lergier, W.
 Helv. Chim. Acta 56, 860-866, 1973

A>Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.

A/Reference number: A01558

A/Accession: A01558

A/Molecule type: protein

A/Residues: 1-11 <STU>

A/Cross-references: UNIPROT:P01290

C/Superfamily: Substance P precursor

C/Keywords: amidated carboxyl end; hormone

F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 21; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	FGIM	4						
Db	8	FGIM	11						

RESULT 3

UN0023
 Substance P - chicken

C:Species: Gallus gallus (chicken)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C/Accession: UN0023

R/Conlon, J.M.; Karsoulis, S.; Schmidt, W.E.; Thim, L.
 Regul. Pept. 20, 171-180, 1988

A>Title: [Arg3]substance P and neuropeptide A from chicken small intestine.

A/Reference number: UN0023; MUID:88204263; PMID:2452461

A/Accession: UN0023

A/Molecule type: protein

A/Residues: 1-11 <CON>

A/Cross-references: UNIPROT:P19850

C/Superfamily: Substance P precursor

C/Keywords: amidated carboxyl end; tachykinin

F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 21; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	FGIM	4						
Db	8	FGIM	11						

RESULT 4

S33300
 probable substance P - smaller spotted catshark

C:Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S33300

R/Waugh, D.; Wang, Y.; Hazon, N.; Balmont, R.J.; Conlon, J.M.
 Eur. J. Biochem. 214, 469-474, 1993

A>Title: Primary structures and biological activities of substance-P-related peptides fr

A/Reference number: S33300; MUID:93392508; PMID:7685693

A/Accession: S33300

A/Molecule type: protein

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: October 26, 2005, 08:05:47 ; Search time 99.5556 Seconds
(without alignments)
16.775 Million cell updates/sec

Title: ~~US-10-053-669-2~~
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 150 summaries

Database ~~US-10-053-669-2~~
Published/Updated: ~~US-10-053-669-2~~
1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppa/PCTUS_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubppa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
8: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
12: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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; CURRENT APPLICATION NUMBER: US/09/265,690C
; NUMBER OF SEQ ID NOS: 4
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; FILE REFERENCE: 2892-106
; CURRENT APPLICATION NUMBER: US/10/230,133
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 09/635,266
; NUMBER OF SEQ ID NOS: 4
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; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: N1427-005
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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83	21	100.0	11	4	US-09-570-022-6 Sequence 6, Appl
84	21	100.0	11	4	US-09-570-022-10 Sequence 10, Appl
85	21	100.0	11	4	US-10-002-593-4 Sequence 4, Appl
86	21	100.0	11	4	US-09-629-642A-1 Sequence 1, Appl
87	21	100.0	11	4	US-10-230-133-1 Sequence 1, Appl
88	21	100.0	11	4	US-09-428-692-21 Sequence 21, Appl
89	21	100.0	11	4	US-09-285-387A-1 Sequence 1, Appl
90	21	100.0	11	5	PCT-US92-06537-1 Sequence 1, Appl
91	21	100.0	11	5	PCT-US95-05600-23 Sequence 23, Appl
92	21	100.0	11	6	5441935-1 Patent No. 5441935
93	21	100.0	11	6	5441935-1 Patent No. 5441935
94	21	100.0	12	1	US-08-441-591-7 Sequence 7, Appl
95	21	100.0	12	1	US-08-303-362A-7 Sequence 7, Appl
96	21	100.0	12	3	US-08-505-250-27 Sequence 27, Appl
97	21	100.0	12	3	US-08-505-250-53 Sequence 53, Appl
98	21	100.0	12	3	US-09-264-709A-16 Sequence 16, Appl
99	21	100.0	12	3	US-08-505-250-27 Sequence 27, Appl
100	21	100.0	12	3	US-08-505-250-53 Sequence 53, Appl

101 21 100.0 12 4 US-09-922-093-2 Sequence 2, Appl1
102 21 100.0 12 4 US-09-922-093-5 Sequence 5, Appl1
103 21 100.0 12 4 US-09-922-093-8 Sequence 8, Appl1
104 21 100.0 12 4 US-09-403-752A-41 Sequence 41, Appl1
105 21 100.0 12 4 US-09-763-669-1 Sequence 1, Appl1
106 21 100.0 12 4 US-09-763-669-2 Sequence 2, Appl1
107 21 100.0 12 4 US-09-625-098F-2 Sequence 2, Appl1
108 21 100.0 12 4 US-09-625-098F-5 Sequence 5, Appl1
109 21 100.0 12 4 US-09-625-098F-8 Sequence 8, Appl1
110 21 100.0 12 4 US-09-428-692-22 Sequence 22, Appl1
111 21 100.0 12 4 US-09-428-692-25 Sequence 25, Appl1
112 21 100.0 12 4 US-09-428-692-28 Sequence 28, Appl1
113 21 100.0 12 4 US-09-551-151A-41 Sequence 41, Appl1
114 21 100.0 12 5 PCT-US92-06532-4 Sequence 4, Appl1
115 21 100.0 12 5 PCT-US95-05600-24 Sequence 24, Appl1
116 21 100.0 13 1 US-07-712-828B-5 Sequence 5, Appl1
117 21 100.0 13 4 US-09-922-093-3 Sequence 3, Appl1
118 21 100.0 13 4 US-09-922-093-6 Sequence 6, Appl1
119 21 100.0 13 4 US-09-922-093-9 Sequence 9, Appl1
120 21 100.0 13 4 US-09-625-098F-3 Sequence 3, Appl1
121 21 100.0 13 4 US-09-625-098F-6 Sequence 6, Appl1
122 21 100.0 13 4 US-09-625-098F-9 Sequence 9, Appl1
123 21 100.0 13 4 US-09-428-692-23 Sequence 23, Appl1
124 21 100.0 13 4 US-09-428-692-26 Sequence 26, Appl1
125 21 100.0 13 4 US-09-428-692-29 Sequence 29, Appl1
126 21 100.0 14 4 US-09-922-093-4 Sequence 4, Appl1
127 21 100.0 14 4 US-09-922-093-7 Sequence 7, Appl1
128 21 100.0 14 4 US-09-922-093-10 Sequence 10, Appl1
129 21 100.0 14 4 US-09-625-098F-4 Sequence 4, Appl1
130 21 100.0 14 4 US-09-625-098F-7 Sequence 7, Appl1
131 21 100.0 14 4 US-09-625-098F-10 Sequence 10, Appl1
132 21 100.0 14 4 US-09-428-692-24 Sequence 24, Appl1
133 21 100.0 14 4 US-09-428-692-27 Sequence 27, Appl1
134 21 100.0 14 4 US-09-428-692-30 Sequence 30, Appl1
135 21 100.0 20 1 US-08-468-514-1 Sequence 1, Appl1
136 21 100.0 20 3 US-08-890-157A-2 Sequence 2, Appl1
137 21 100.0 20 3 US-08-505-250-50 Sequence 50, Appl1
138 21 100.0 20 3 US-08-505-250-50 Sequence 50, Appl1
139 21 100.0 20 4 US-09-570-022-23 Sequence 23, Appl1
140 21 100.0 21 1 US-08-468-514-4 Sequence 4, Appl1
141 21 100.0 22 1 US-08-468-514-11 Sequence 11, Appl1
142 21 100.0 61 4 US-09-270-767-363A8 Sequence 363A8, A
143 21 100.0 61 4 US-09-270-767-51565 Sequence 51565, A
144 21 100.0 65 4 US-09-148-545-171 Sequence 171, A
145 21 100.0 68 4 US-09-902-540-11170 Sequence 11170, A
146 21 100.0 70 4 US-09-248-796A-25823 Sequence 25823, A
147 21 100.0 72 4 US-09-489-039A-11664 Sequence 11664, A
148 21 100.0 73 4 US-09-949-016-92299 Sequence 92299, Ap
149 21 100.0 78 3 US-09-134-001C-3647 Sequence 3647, Ap
150 21 100.0 78 4 US-09-540-236-2303 Sequence 2303, Ap

ALIGNMENTS

RESULT 1
US-08-441-591-63
; Sequence 63, Application US/08441591
; Patent No. 5637682
; GENERAL INFORMATION:
; APPLICANT: NIEWLANDT, D., GOLD, L. AND WECKER, M.
; TITLE OF INVENTION: HIGH-AFFINITY
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO THE TACHYKININ
; TITLE OF INVENTION: SUBSTANCE P
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,591
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/303,362
; APPLICATION DATE: 9-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX21/C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-441-591-63
Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FGLM 4
Db 1 FGLM 4

RESULT 2
US-08-303-362A-63
; Sequence 63, Application US/08303362A
; Patent No. 5648214
; GENERAL INFORMATION:
; APPLICANT: NIEWLANDT, D., GOLD, L. AND WECKER, M.
; TITLE OF INVENTION: HIGH-AFFINITY
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO THE TACHYKININ
; TITLE OF INVENTION: SUBSTANCE P
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS

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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:00:50 ; Search time 57.7778 Seconds
(without alignments)
26.776 Million cell updates/sec

Title: us-10-053-669-2

Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match -0%
Maximum Match 100%
Listing first 150 summaries

Date/Time: 10/26/2005 10:59:50
1: geneseqp19808:.*
2: geneseqp19808:.*
3: geneseqp20008:.*
4: geneseqp20008:.*
5: geneseqp20028:.*
6: geneseqp20038:.*
7: geneseqp20038:.*
8: geneseqp20048:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	2 AAW41683	AAW41683 Peptide u
2	21	100.0	4	2 AAY31075	AAY31075 Non-cross
3	21	100.0	4	3 AAB23026	AAB23026 Human/rat
4	21	100.0	4	3 AAY67577	AAY67577 P antigen
5	21	100.0	4	4 AAB91447	AAB91447 Tachykinin
6	21	100.0	4	4 AAB10091	AB10091 Substance
7	21	100.0	4	5 AAU77846	AAU77846 Tachykinin
8	21	100.0	4	5 ADE94198	ADE94198 High acti
9	21	100.0	4	8 ADR43772	ADR43772 Human mag
10	21	100.0	5	2 AAR33009	AAR33009 Alpha-sub
11	21	100.0	5	2 AAR33008	AAR33008 Alpha-sub
12	21	100.0	5	2 AAR33007	AAR33007 Alpha-sub
13	21	100.0	5	2 AAR33010	AAR33010 Alpha-sub
14	21	100.0	5	2 AAR54549	AAR54549 Cholecyt
15	21	100.0	5	2 AAR54541	AAR54541 Cholecyt
16	21	100.0	5	2 AAR54550	AAR54550 Cholecyt
17	21	100.0	5	2 AAR54548	AAR54548 Cholecyt
18	21	100.0	5	2 AAR54547	AAR54547 Tetrapt
19	21	100.0	5	2 AAY96443	AAY96443 Substance
20	21	100.0	5	2 AAY50325	AAY50325 Neutrophil
21	21	100.0	5	2 AAW92702	AAW92702 Human tac
22	21	100.0	5	2 AAB23025	AAB23025 Human/rat
23	21	100.0	5	3 AAY67576	AAY67576 P antigen
24	21	100.0	5	4 AAB91428	AAB91428 Tachykinin
25	21	100.0	5	4 AAB91428	AAB91428 Tachykinin

26	21	100.0	5	4 AAB91389	AAB91389 Tachykinin
27	21	100.0	5	5 AAB10090	AB10090 Substance
28	21	100.0	5	5 AAB10089	AB10089 Substance
29	21	100.0	5	5 AAB10088	AB10088 Substance
30	21	100.0	5	5 AAU77845	AAU77845 Tachykinin
31	21	100.0	5	7 ADE94205	ADE94205 High acti
32	21	100.0	5	7 ADE94203	ADE94203 High acti
33	21	100.0	5	7 ADE94204	ADE94204 High acti
34	21	100.0	5	7 ADF92530	ADF92530 Substance
35	21	100.0	5	8 ADR95078	ADR95078 Mammalian
36	21	100.0	5	8 ADR95078	ADR95078 E. coli m
37	21	100.0	5	8 ADR43771	ADR43771 Human mag
38	21	100.0	6	1 AAP40519	AAP40519 Sequence
39	21	100.0	6	1 AAP50694	AAP50694 Sequence
40	21	100.0	6	1 AAP50632	AAP50632 Substance
41	21	100.0	6	1 AAP61486	AAP61486 Peptide h
42	21	100.0	6	2 AAR07893	AAR07893 Cyclicopept
43	21	100.0	6	2 AAR07893	AAR07893 Cyclicopept
44	21	100.0	6	2 AAR21959	AAR21959 Substance
45	21	100.0	6	2 AAR27690	AAR27690 Cyclic ta
46	21	100.0	6	2 AAR27694	AAR27694 Cyclic ta
47	21	100.0	6	2 AAR27691	AAR27691 Cyclic ta
48	21	100.0	6	2 AAW9692	AAW9692 Substance
49	21	100.0	6	2 AAW9686	AAW9686 Substance
50	21	100.0	6	2 AAW92706	AAW92706 Human tac
51	21	100.0	6	2 AAW92659	AAW92659 Human tac
52	21	100.0	6	3 AAB03356	AAB03356 Neurokinin
53	21	100.0	6	3 AAY67575	AAY67575 P antigen
54	21	100.0	6	3 AAY97917	AAY97917 Neurokinin
55	21	100.0	6	3 AAY97947	AAY97947 Neurokinin
56	21	100.0	6	3 AAY97932	AAY97932 Neurokinin
57	21	100.0	6	4 AAB82453	AAB82453 Fluorinat
58	21	100.0	6	4 AAB82436	AAB82436 Fluorinat
59	21	100.0	6	4 AAB91421	AB91421 Tachykinin
60	21	100.0	6	4 AAB91425	AB91425 Tachykinin
61	21	100.0	6	4 AAB91390	AB91390 Tachykinin
62	21	100.0	6	4 AAB91419	AB91419 Tachykinin
63	21	100.0	6	4 AAG99351	AAG99351 Atypical
64	21	100.0	6	4 AAU07303	AAU07303 Neurokinin
65	21	100.0	6	4 AAB68998	AAB68998 Neurokinin
66	21	100.0	6	4 AAB88884	AAB88884 Chimeric
67	21	100.0	6	4 AAB88886	AAB88886 Chimeric
68	21	100.0	6	4 AAG67862	AAG67862 Neurokinin
69	21	100.0	6	5 AAB10086	AB10086 Substance
70	21	100.0	6	7 ADB88521	ADB88521 Human NK-
71	21	100.0	6	7 ADE94202	ADE94202 High acti
72	21	100.0	6	7 ADG39528	ADG39528 Neurokinin
73	21	100.0	7	2 AAR21956	AAR21956 Substance
74	21	100.0	7	2 AAY50324	AAY50324 Neutrophil
75	21	100.0	7	2 AAW92662	AAW92662 Human tac
76	21	100.0	7	2 AAW92705	AAW92705 Human tac
77	21	100.0	7	3 AAY67574	AAY67574 P antigen
78	21	100.0	7	3 AAB80323	AB80323 Human pro
79	21	100.0	7	4 AAB80324	AB80324 Human pro
80	21	100.0	7	4 AAB91431	AB91431 Tachykinin
81	21	100.0	7	4 AAB91420	AB91420 Tachykinin
82	21	100.0	7	4 AAG93350	AAG93350 Atypical
83	21	100.0	7	4 AAB88845	AAB88845 Chimeric
84	21	100.0	7	5 AAB80950	AB80950 Substance
85	21	100.0	7	5 ADE94201	ADE94201 High acti
86	21	100.0	7	7 ADF92529	ADF92529 Substance
87	21	100.0	7	8 ADR95077	ADR95077 Mammalian
88	21	100.0	8	1 AAP20303	AAP20303 Gastroint
89	21	100.0	8	2 AAR28444	AAR28444 Neurokinin
90	21	100.0	8	2 AAW92664	AAW92664 Human tac
91	21	100.0	8	2 AAW92710	AAW92710 Human tac
92	21	100.0	8	3 AAY67573	AAY67573 P antigen
93	21	100.0	8	4 AAB91407	AB91407 Tachykinin
94	21	100.0	8	4 AAB91416	AB91416 Tachykinin
95	21	100.0	8	4 AAB91424	AB91424 Tachykinin
96	21	100.0	8	4 AAG99349	AAG99349 Atypical
97	21	100.0	8	5 AAB909498	AB909498 Substance
98	21	100.0	8	5 AAB909498	AB909498 Substance

99	21	100.0	8	7	ADB94200	Ad994200 High acti
100	21	100.0	9	1	AAW50634	AAW50634 Substance
101	21	100.0	9	2	AAW92714	AAW92714 Human tac
102	21	100.0	9	4	AAW80325	AAW80325 Human pro
103	21	100.0	9	4	AAW91446	AAW91446 Tachykin
104	21	100.0	9	4	AAW91369	AAW91369 Tachykin
105	21	100.0	9	4	AAW99348	AAW99348 Aclycal
106	21	100.0	9	7	AAW38833	AAW38833 Membrane
107	21	100.0	9	7	ADW92528	ADW92528 Substance
108	21	100.0	9	8	ADW04477	ADW04477 Substance
109	21	100.0	9	8	ADW95076	ADW95076 Mammalian
110	21	100.0	9	8	ADW15335	ADW15335 Substance
111	21	100.0	10	1	AAW50633	AAW50633 Substance
112	21	100.0	10	2	AAW21933	AAW21933 Substance
113	21	100.0	10	2	AAW65181	AAW65181 S. cerevi
114	21	100.0	10	2	AAW99684	AAW99684 Substance
115	21	100.0	10	2	AAW06939	AAW06939 Substance
116	21	100.0	10	2	AAW92663	AAW92663 Human tac
117	21	100.0	10	4	AAW66675	AAW66675 Tachykin
118	21	100.0	10	4	AAW91445	AAW91445 Tachykin
119	21	100.0	10	4	AAW93447	AAW93447 Aclycal
120	21	100.0	10	4	AAW64746	AAW64746 Substance
121	21	100.0	10	8	ADW12181	ADW12181 Antino aci
122	21	100.0	10	8	ADW27868	ADW27868 Trichomon
123	21	100.0	11	1	AAW61480	AAW61480 Sequence
124	21	100.0	11	1	AAW80312	AAW80312 Sequence
125	21	100.0	11	2	AAW11854	AAW11854 Undecapep
126	21	100.0	11	2	AAW13162	AAW13162 Sialic ac
127	21	100.0	11	2	AAW28442	AAW28442 Substance
128	21	100.0	11	2	AAW21969	AAW21969 Cyclic su
129	21	100.0	11	2	AAW21942	AAW21942 Substance
130	21	100.0	11	2	AAW21962	AAW21962 Substance
131	21	100.0	11	2	AAW21945	AAW21945 Substance
132	21	100.0	11	2	AAW21963	AAW21963 Substance
133	21	100.0	11	2	AAW21949	AAW21949 Substance
134	21	100.0	11	2	AAW21951	AAW21951 Substance
135	21	100.0	11	2	AAW21934	AAW21934 Substance
136	21	100.0	11	2	AAW21946	AAW21946 Substance
137	21	100.0	11	2	AAW21964	AAW21964 Substance
138	21	100.0	11	2	AAW21970	AAW21970 Cyclic su
139	21	100.0	11	2	AAW21938	AAW21938 Substance
140	21	100.0	11	2	AAW21941	AAW21941 Substance
141	21	100.0	11	2	AAW21943	AAW21943 Substance
142	21	100.0	11	2	AAW21954	AAW21954 Substance
143	21	100.0	11	2	AAW42646	AAW42646 Neurokin
144	21	100.0	11	2	AAW85243	AAW85243 Substance
145	21	100.0	11	2	AAW77310	AAW77310 Substance
146	21	100.0	11	2	AAW33181	AAW33181 Mono-DTPA
147	21	100.0	11	2	AAW33180	AAW33180 Mono-DTPA
148	21	100.0	11	2	AAW04616	AAW04616 Substance
149	21	100.0	11	2	AAW79775	AAW79775 Substance
150	21	100.0	11	2	AAW42973	AAW42973 Substrate

ALIGNMENTS

RESULT 1
AAW41683
ID AAW41683 standard; peptide; 4 AA.
XX AAW41683;
AC AAW41683;
XX 09-JUN-1998 (first entry)
DT 09-JUN-1998 (first entry)
XX Peptide used in ophthalmic drug to treat corneal disorders.
DE Peptide used in ophthalmic drug to treat corneal disorders.
XX Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;
KW keratitis; insulin like growth factor-I; IGF-I; eye drop.
XX Synthetic.
OS Synthetic.
XX Key Location/Qualifiers
PH Key Location/Qualifiers

FT Modified-site 4 /note= "C-terminal amide"
FT
XX
XX
PN WO9749419-A1.
XX
XX
PD 31-DEC-1997.
XX
XX
PF 11-JUN-1997; 97WO-JP002015.
XX
XX
PR 26-JUN-1996; 96JP-00165612.
XX
XX
PA (SANT) SANTEN PHARM CO LTD.
XX
XX
PI Nishida T, Nakamura M, Nakata K;
XX
XX
DR WPI; 1998-076907/07.
XX
XX
PT Ophthalmic drug composition containing tetrapeptide - is useful as
PT corneal disorder remedy for corneal ulcer, corneal epithelial peeling,
PT dry eye, keratitis.
XX
XX
PS Claim 1; Page 15; 19pp; Japanese.
XX
XX
CC The present sequence represents a tetrapeptide which is the active
CC ingredient in an ophthalmic drug composition. It is used, together with
CC insulin like growth factor-I (IGF-I), to treat corneal disorders such as
CC corneal ulcer, corneal epithelial peeling, dry eye and keratitis. The
CC dosage is 0.1-5000 (preferably 1-1000) mg/day of the tetrapeptide and
CC 0.001-100 (preferably 0.01-10) mg/day of IGF-I. The preferable form of
CC the composition is eye drops
XX
XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FGLM 4
DB 1 FGLM 4
RESULT 2
AAW31075
ID AAW31075 standard; peptide; 4 AA.
XX AAW31075;
AC AAW31075;
XX 21-OCT-1999 (first entry)
DT 21-OCT-1999 (first entry)
XX
XX
DE Non-crosslinked protein particle peptide 124.
XX
XX
KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
KW albumin; haemoglobin; nanometer; micrometer; clearance.
XX
XX
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 4 /note= "C-terminal amide"
FT
XX
XX
PN US5945033-A.
XX
XX
PD 31-AUG-1999.
XX
XX
PF 12-NOV-1996; 96US-00747137.
XX
XX
PR 15-JAN-1991; 91US-00641720.
PR 13-OCT-1992; 92US-00959560.
PR 01-JUN-1993; 93US-0069831.
PR 14-MAR-1994; 94US-00212546.
XX
XX
PA (HEMO-) HEMOSPHERE INC.

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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:12:17 ; Search time 99.556 Seconds
(without alignment)
20.575 Million cell updates/sec

Title: us-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3223

Minimum (DB-seq-length): 0
Maximum (DB-seq-length): 11

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 150 summaries

Database :
1: uniprot_03:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	11	1	TKN4_PSEGU
2	21	100.0	11	1	TKN5_PSEGU
3	21	100.0	11	1	TKNA_CAYPO
4	21	100.0	11	1	TKNA_CHICK
5	21	100.0	11	1	TKNA_HORSE
6	21	100.0	11	1	TKNA_ONCMY
7	21	100.0	11	1	TKNA_SCYCA
8	18	85.7	10	1	TKN1_SCYCA
9	18	85.7	10	1	TKNB_RANCA
10	18	85.7	10	1	TKS1_AEDAE
11	18	85.7	10	1	TKS2_AEDAE
12	18	85.7	11	1	TKN1_UPEIN
13	18	85.7	11	1	TKN1_UPEIN
14	18	85.7	11	1	TKN2_UPEIN
15	18	85.7	11	1	TKNA_RANCA
16	18	85.7	11	1	TKNA_RANCA
17	18	85.7	11	1	TKN_PHYFU
18	18	85.7	11	1	TKN_PHYFU
19	16	76.2	5	1	ALL4_CARMA
20	16	76.2	7	1	ALL2_CARMA
21	16	76.2	7	1	ALL3_CARMA
22	16	76.2	7	1	ALL4_CARMA
23	16	76.2	7	1	ALL5_CARMA
24	16	76.2	7	1	ALL7_CARMA
25	16	76.2	8	1	ALL2_CARMA
26	16	76.2	8	1	ALL5_CARMA
27	16	76.2	8	1	ALL7_CARMA
28	16	76.2	8	1	ALL8_CARMA
29	16	76.2	8	1	ALL1_CARMA
30	16	76.2	8	1	ALL3_CARMA
31	16	76.2	8	1	ALL4_CARMA

32	16	76.2	8	1	ALL4_CARMA	P82155 cydia pomon
33	16	76.2	8	1	ALL5_CARMA	P82156 cydia pomon
34	16	76.2	8	1	ALL6_CARMA	P82157 cydia pomon
35	16	76.2	8	1	ALL7_CARMA	P81809 carcius ma
36	16	76.2	8	1	ALL8_CARMA	P81811 carcius ma
37	16	76.2	8	1	ALL9_CARMA	P81813 carcius ma
38	16	76.2	9	1	ALL10_CARMA	P81813 carcius ma
39	16	76.2	9	1	ALL11_CARMA	P81813 carcius ma
40	16	76.2	9	2	ALL12_CARMA	P81822 carcius ma
41	16	76.2	10	1	ALL13_CARMA	P81822 carcius ma
42	16	76.2	10	2	ALL14_CARMA	P81822 carcius ma
43	16	76.2	10	2	ALL15_CARMA	P81822 carcius ma
44	16	76.2	10	2	ALL16_CARMA	P81822 carcius ma
45	16	76.2	10	2	ALL17_CARMA	P81822 carcius ma
46	16	76.2	10	2	ALL18_CARMA	P81822 carcius ma
47	16	76.2	10	2	ALL19_CARMA	P81822 carcius ma
48	16	76.2	10	2	ALL20_CARMA	P81822 carcius ma
49	16	76.2	10	2	ALL21_CARMA	P81822 carcius ma
50	16	76.2	10	2	ALL22_CARMA	P81822 carcius ma
51	16	76.2	10	2	ALL23_CARMA	P81822 carcius ma
52	16	76.2	10	2	ALL24_CARMA	P81822 carcius ma
53	16	76.2	10	2	ALL25_CARMA	P81822 carcius ma
54	16	76.2	10	2	ALL26_CARMA	P81822 carcius ma
55	16	76.2	10	2	ALL27_CARMA	P81822 carcius ma
56	16	76.2	10	2	ALL28_CARMA	P81822 carcius ma
57	16	76.2	10	2	ALL29_CARMA	P81822 carcius ma
58	16	76.2	10	2	ALL30_CARMA	P81822 carcius ma
59	16	76.2	10	2	ALL31_CARMA	P81822 carcius ma
60	16	76.2	10	2	ALL32_CARMA	P81822 carcius ma
61	16	76.2	10	2	ALL33_CARMA	P81822 carcius ma
62	16	76.2	10	2	ALL34_CARMA	P81822 carcius ma
63	16	76.2	10	2	ALL35_CARMA	P81822 carcius ma
64	16	76.2	10	2	ALL36_CARMA	P81822 carcius ma
65	16	76.2	10	2	ALL37_CARMA	P81822 carcius ma
66	16	76.2	10	2	ALL38_CARMA	P81822 carcius ma
67	16	76.2	10	2	ALL39_CARMA	P81822 carcius ma
68	16	76.2	10	2	ALL40_CARMA	P81822 carcius ma
69	16	76.2	10	2	ALL41_CARMA	P81822 carcius ma
70	16	76.2	10	2	ALL42_CARMA	P81822 carcius ma
71	16	76.2	10	2	ALL43_CARMA	P81822 carcius ma
72	16	76.2	10	2	ALL44_CARMA	P81822 carcius ma
73	16	76.2	10	2	ALL45_CARMA	P81822 carcius ma
74	16	76.2	10	2	ALL46_CARMA	P81822 carcius ma
75	16	76.2	10	2	ALL47_CARMA	P81822 carcius ma
76	16	76.2	10	2	ALL48_CARMA	P81822 carcius ma
77	16	76.2	10	2	ALL49_CARMA	P81822 carcius ma
78	16	76.2	10	2	ALL50_CARMA	P81822 carcius ma
79	16	76.2	10	2	ALL51_CARMA	P81822 carcius ma
80	16	76.2	10	2	ALL52_CARMA	P81822 carcius ma
81	16	76.2	10	2	ALL53_CARMA	P81822 carcius ma
82	16	76.2	10	2	ALL54_CARMA	P81822 carcius ma
83	16	76.2	10	2	ALL55_CARMA	P81822 carcius ma
84	16	76.2	10	2	ALL56_CARMA	P81822 carcius ma
85	16	76.2	10	2	ALL57_CARMA	P81822 carcius ma
86	16	76.2	10	2	ALL58_CARMA	P81822 carcius ma
87	16	76.2	10	2	ALL59_CARMA	P81822 carcius ma
88	16	76.2	10	2	ALL60_CARMA	P81822 carcius ma
89	16	76.2	10	2	ALL61_CARMA	P81822 carcius ma
90	16	76.2	10	2	ALL62_CARMA	P81822 carcius ma
91	16	76.2	10	2	ALL63_CARMA	P81822 carcius ma
92	16	76.2	10	2	ALL64_CARMA	P81822 carcius ma
93	16	76.2	10	2	ALL65_CARMA	P81822 carcius ma
94	16	76.2	10	2	ALL66_CARMA	P81822 carcius ma
95	16	76.2	10	2	ALL67_CARMA	P81822 carcius ma
96	16	76.2	10	2	ALL68_CARMA	P81822 carcius ma
97	16	76.2	10	2	ALL69_CARMA	P81822 carcius ma
98	16	76.2	10	2	ALL70_CARMA	P81822 carcius ma
99	16	76.2	10	2	ALL71_CARMA	P81822 carcius ma
100	16	76.2	10	2	ALL72_CARMA	P81822 carcius ma
101	16	76.2	10	2	ALL73_CARMA	P81822 carcius ma
102	16	76.2	10	2	ALL74_CARMA	P81822 carcius ma
103	16	76.2	10	2	ALL75_CARMA	P81822 carcius ma
104	16	76.2	10	2	ALL76_CARMA	P81822 carcius ma

105	12	57.1	9	2	Q7ZPJ3	Q7ZPJ3 human immun
106	12	57.1	9	2	Q7ZPJ5	Q7ZPJ5 human immun
107	12	57.1	9	2	Q7ZPJ7	Q7ZPJ7 human immun
108	12	57.1	9	2	Q7ZPK1	Q7ZPK1 human immun
109	12	57.1	10	1	CU30.LOCMI	P11735 locusta mig
110	12	57.1	10	1	DYS2.LIMDU	P82080 limodysnae
111	12	57.1	10	1	DYS6.LIMSA	P82084 limodysnae
112	12	57.1	10	1	RT02.BOVIN	P82923 bos taurus
113	12	57.1	10	1	TKU2.URGUN	P40752 urechis uni
114	12	57.1	10	1	Q7KZ59	Q7KZ59 homo sapien
115	12	57.1	10	2	Q25355	Q25355 locusta mig
116	12	57.1	10	2	Q25356	Q25356 locusta mig
117	12	57.1	10	2	Q85V65	Q85V65 eucalyptus
118	12	57.1	10	2	Q8SAC2	Q8SAC2 amblystegiu
119	12	57.1	10	2	Q7M111	Q7M111 phaseolus v
120	12	57.1	10	2	Q9S905	Q9S905 glycine max
121	12	57.1	10	2	Q9AE19	Q9AE19 streptococc
122	12	57.1	10	2	Q9R7J8	Q9R7J8 helicobacte
123	12	57.1	10	2	Q6LCT8	Q6LCT8 rattus norv
124	12	57.1	10	2	Q71VN2	Q71VN2 mus musculu
125	12	57.1	10	2	Q8JFE7	Q8JFE7 ficedula al
126	12	57.1	10	2	Q8JFE7	Q8JFE7 ficedula al
127	12	57.1	10	2	Q8J3J3	Q8J3J3 ficedula by
128	12	57.1	11	1	PVK1.BLACR	P83923 blaberus cr
129	12	57.1	11	1	PVK1.BLADU	P83924 blaptica du
130	12	57.1	11	1	PVK1.GROPO	P83925 leucophaea
131	12	57.1	11	1	PVK1.LETMA	P83922 nauphoeta c
132	12	57.1	11	1	PVK1.NAUCI	P82074 litorea rub
133	12	57.1	11	1	RE41.LITRU	Q9UC46 homo sapien
134	12	57.1	11	2	Q9UC46	Q9UC46 litorea s
135	12	57.1	11	2	Q6UZ55	Q6UZ55 plasmodium
136	12	57.1	11	2	Q7RH63	Q7RH63 sus scrofa
137	12	57.1	11	2	Q9TRX0	Q9TRX0 oreochromis
138	12	57.1	11	2	Q7R871	Q7R871 oreochromis
139	12	57.1	11	2	Q7R872	Q7R872 oreochromis
140	12	57.1	11	2	Q7R873	Q7R873 oreochromis
141	12	57.1	11	2	Q34380	Q34380 drosophila
142	12	57.1	11	2	Q6RWV4	Q6RWV4 eubacterium
143	12	57.1	11	2	Q7M1A0	Q7M1A0 eubacterium
144	12	57.1	11	2	Q7M1D1	Q7M1D1 unidentified
145	12	57.1	11	2	Q9E2U3	Q9E2U3 escherichia
146	11	52.4	7	2	Q9CSB3	Q9CSB3 arbidopsis
147	11	52.4	8	1	CAD1.ENTFA	P13268 enterococcu
148	11	52.4	8	1	DYS4.LIMSA	P82082 limodysnae
149	11	52.4	8	1	DYS5.LIMSA	P82083 limodysnae
150	11	52.4	8	1	RT34.BOVIN	P82929 bos taurus

ALIGNMENTS

RESULT 1
TKN4_PSECU STANDARD; PRT; 11 AA.

AC P42959;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Substance P-like peptide I (PG-SP1).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN (1)
RP SEQUENCE
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.,
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.",
RL Peptides 11:299-304(1990).

CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secreteagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR; E60409.
DR InterPro; IPR002040; Tachy Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing;
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
FT MOD RES 1 1
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1A57 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 8 FGLM 11

RESULT 2

TKN5_PSECU STANDARD; PRT; 11 AA.

AC P42950;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Substance P-like peptide II (PG-SPII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN (1)
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.,
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.",
RL Peptides 11:299-304(1990).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secreteagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR; F60409; F60409.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing;
KW Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
FT MOD RES 1 1
FT MOD RES 11 11
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1A57 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGLM 4
DB 8 FGLM 11

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 26, 2005, 08:12:37 ; Search time 20.444 Seconds
(without alignments)
18.825 Million cell updates/sec

Title: UB-10-053-669-2
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1328

Minimum DB-seq-length: 0
Maximum DB-seq-length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 150 summaries

Database :
1: p1r1:*
3: p1r2:*
4: p1r3:*
5: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	11	1 A60654	substance P - guin
2	21	100.0	11	1 SPHO	substance P - hors
3	21	100.0	11	1 JN0023	substance P - chic
4	21	100.0	11	2 S33300	probable substance
5	21	100.0	11	2 E60409	substance P-like P
6	21	100.0	11	2 F60409	substance P-like P
7	21	100.0	11	2 S23308	substance P - rain
8	18	85.7	10	2 B49581	substance P - rain
9	18	85.7	10	2 A49581	substance P - rain
10	18	85.7	10	2 A24867	substance P - rain
11	18	85.7	10	2 B61033	substance P - rain
12	18	85.7	11	2 S07203	substance P - rain
13	18	85.7	11	2 S07201	substance P - rain
14	18	85.7	11	2 A61033	substance P - rain
15	16	76.2	8	2 D47353	substance P - rain
16	16	76.2	10	2 B60527	substance P - rain
17	16	76.2	10	2 B60589	substance P - rain
18	15	71.4	5	2 PT0278	substance P - rain
19	15	71.4	10	1 SPPGK	substance P - rain
20	15	71.4	10	2 JN0024	substance P - rain
21	15	71.4	10	2 S06964	substance P - rain
22	15	71.4	10	2 S23307	substance P - rain
23	15	71.4	10	2 S23307	substance P - rain
24	15	71.4	10	2 S23307	substance P - rain
25	15	71.4	10	2 S07202	substance P - rain
26	15	71.4	10	2 C61033	substance P - rain
27	15	71.4	10	2 S27178	substance P - rain
28	15	71.4	11	1 E00C	substance P - rain
29	15	71.4	11	1 E00CC	substance P - rain

30	15	71.4	11	2 C60409	kassinin-like pept
31	15	71.4	11	2 B60409	kassinin-like pept
32	15	71.4	11	2 B60409	kassinin-like pept
33	15	71.4	11	2 S23306	substance P - Acta
34	14	66.7	5	2 A44955	alkanal monooxygen
35	14	66.7	8	2 B47393	neuropeptide calia
36	13	61.9	8	2 PH1618	Ig H chain V-D-J r
37	13	61.9	8	2 PC4373	telomeric and tetr
38	13	61.9	9	2 PT0225	Ig heavy chain CDR
39	13	61.9	9	2 PH1591	Ig H chain V-D-J r
40	13	61.9	10	1 RHPCG	gonadolibertin - pi
41	13	61.9	10	1 RHSHG	gonadolibertin - sh
42	13	61.9	10	1 RHAGI	gonadolibertin I -
43	13	61.9	10	2 PT0230	Ig heavy chain CDR
44	13	61.9	10	2 PH1633	Ig H chain V-D-J r
45	13	61.9	10	2 A59173	nuclease Bnl (EC 3
46	13	61.9	11	2 A57458	gene Gax protein -
47	13	61.9	11	4 PC2124	amino transferase C
48	12	57.1	7	1 A61324	dermorphin - Rohde
49	12	57.1	7	2 S36662	dermorphin (Lys-7)
50	12	57.1	7	2 A40504	hypothetical prote
51	12	57.1	8	2 PH0803	T-cell receptor al
52	12	57.1	8	2 S11078	glucose-6-phosphat
53	12	57.1	9	2 D24180	fibritinogen beta ch
54	12	57.1	9	2 F28854	fibritinopeptide B -
55	12	57.1	9	2 PH0942	T-cell receptor be
56	12	57.1	9	2 G58502	kidney and bladder
57	12	57.1	9	2 PT0080	60K Ca binding pro
58	12	57.1	9	2 PC7074	translation elonga
59	12	57.1	9	2 S18850	vitamin D3 26-mono
60	12	57.1	10	2 PT0310	Ig heavy chain CRD
61	12	57.1	10	2 PH0807	T-cell receptor al
62	12	57.1	10	2 S38305	lectin GNL2 alpha
63	12	57.1	11	2 PT0250	Ig heavy chain CRD
64	12	57.1	11	2 S57575	T-cell receptor V-
65	12	57.1	11	2 C58501	42K bile stone pro
66	12	57.1	11	2 A44755	20alpha-hydroxyste
67	11	52.4	5	2 A61445	Met-enkephalin - b
68	11	52.4	7	2 A60224	Met-enkephalin-Arg
69	11	52.4	9	2 A11497	transaldolase (EC
70	11	52.4	9	2 D44787	calliFERamide 13
71	11	52.4	9	2 I49406	bone gla protein -
72	11	52.4	10	1 GMROL2	leucosulfakinin-II
73	11	52.4	10	2 B60656	leucosulfakinin II
74	11	52.4	11	1 GMROL	leucosulfakinin -
75	11	52.4	11	2 A40693	transgelin - sheep
76	11	52.4	11	2 PT0249	Ig heavy chain CRD
77	11	52.4	11	2 A60656	perisulfakinin - A
78	10	47.6	4	2 PT0240	Ig heavy chain CRD
79	10	47.6	4	2 A53284	T-cell receptor be
80	10	47.6	5	2 A44817	27.5 kda structura
81	10	47.6	5	2 I44817	27.5K structural p
82	10	47.6	5	2 E44817	27.5K structural p
83	10	47.6	5	2 A44817	28.5K structural p
84	10	47.6	5	2 A44817	28K structural pro
85	10	47.6	6	2 B56979	collagen alpha 1(I)
86	10	47.6	6	2 PT0643	T-cell receptor be
87	10	47.6	6	2 PT0718	T-cell receptor be
88	10	47.6	6	2 PT0589	T-cell receptor be
89	10	47.6	6	2 PT0727	T-cell receptor be
90	10	47.6	7	2 PT0246	Ig heavy chain CRD
91	10	47.6	7	2 A11483	aspartate transami
92	10	47.6	7	2 PT0663	T-cell receptor be
93	10	47.6	7	2 T09512	NADH2 dehydrogenas
94	10	47.6	7	2 S09066	globulin IV alpha
95	10	47.6	7	2 PT0529	T-cell receptor be
96	10	47.6	7	4 PC2056	trichodecenen II -
97	10	47.6	7	4 PC2057	trichodecenen II -
98	10	47.6	8	2 PA0032	Ig gamma chain C r
99	10	47.6	8	2 PT0627	T-cell receptor be
100	10	47.6	8	2 PT0522	T-cell receptor be
101	10	47.6	8	2 PT0522	T-cell receptor be
102	10	47.6	2	2 PT0559	T-cell receptor be

103	10	47.6	8	2	PT0554	T-cell receptor be
104	10	47.6	8	2	PT0725	T-cell receptor be
105	10	47.6	8	2	PC4372	telomeric and tetr
106	10	47.6	8	2	A37521	R-phycocerythrin ga
107	10	47.6	8	2	F60588	sperm-activating p
108	10	47.6	8	2	E60588	sperm-activating p
109	10	47.6	8	2	G60588	sperm-activating p
110	10	47.6	8	4	IS5411	hypothetical histo
111	10	47.6	9	2	A61230	caldesquestrin, car
112	10	47.6	9	2	E28854	fibrinopeptide B -
113	10	47.6	9	2	D28854	23k exantigen -
114	10	47.6	9	2	B33098	collagen alpha 2(V
115	10	47.6	9	2	S65855	glycine cleavage s
116	10	47.6	9	2	FS0253	118k stomach cance
117	10	47.6	9	2	A60356	alpha-2-macroglobu
118	10	47.6	10	1	ECLQJM	tachykinin I - mig
119	10	47.6	10	1	ECLQJM	tachykinin III - m
120	10	47.6	10	2	PN0136	pepsin (EC 3.4.23.
121	10	47.6	10	2	PN0136	angiotensin I - Ja
122	10	47.6	10	2	A60624	inhibin beta-A cha
123	10	47.6	10	2	S10926	seed storage prote
124	10	47.6	10	2	C38925	hypothetical prote
125	10	47.6	10	2	A35556	inhibin beta-B cha
126	10	47.6	10	2	B24736	cartilage oligomer
127	10	47.6	10	2	S66214	T-cell receptor be
128	10	47.6	10	2	PT0632	T-cell receptor be
129	10	47.6	10	2	PT0664	cytochrome-c oxida
130	10	47.6	10	2	S43630	angiotensin precu
131	10	47.6	10	2	A90917	sperm-activating p
132	10	47.6	10	2	G60787	sperm-activating p
133	10	47.6	10	2	E60787	sperm-activating p
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139	10	47.6	10	2	E60527	sperm-activating p
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145	10	47.6	11	1	ECLQ2M	tachykinin II - ml
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148	10	47.6	11	2	S70720	trigger factor hom
149	10	47.6	11	2	I33098	173k exantigen -
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ALIGNMENTS

RESULT 1
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 Substance P - guinea pig
 C/Species: Cavia porcellus (guinea pig)
 C/Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C/Accession: A60654
 R/Murphy, R.
 Neuropeptides 14, 105-110, 1989
 A/Title: Primary amino acid sequence of guinea-pig substance P.
 A/Reference number: A60654; MUID:90044685; PMID:2478925
 A/Accession: A60654
 A/Molecule type: protein
 A/Residues: 1-11 <MUR>
 A/Cross-references: UNIPROT:P01290
 C/Superfamily: substance P precursor
 C/Keywords: amidated carboxyl end; neuropeptide; tachykinin
 F/11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 21; DB 1; Length 11;
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 8 FGLM 11

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 C/Species: Equus caballus (domestic horse)
 C/Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
 C/Accession: A01558
 R/Studer, R.O.; Tizzeck, A.; Lergier, W.
 Heiv. Chim. Acta 56, 860-866, 1973
 A/Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.
 A/Reference number: A01558
 A/Accession: A01558
 A/Molecule type: protein
 A/Residues: 1-11 <STU>
 A/Cross-references: UNIPROT:P01290
 C/Superfamily: substance P precursor
 C/Keywords: amidated carboxyl end; hormone
 F/11/Modified site: amidated carboxyl end (Met) #status experimental

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 Db 8 FGLM 11

RESULT 3
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 C/Species: Gallus gallus (chicken)
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C/Accession: JN0023
 R/Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
 Regul. Pept. 20, 171-180, 1988
 A/Title: [Arg3]substance P and neurokinin A from chicken small intestine.
 A/Reference number: JN0023; MUID:88204263; PMID:2452461
 A/Accession: JN0023
 A/Molecule type: protein
 A/Residues: 1-11 <CON>
 A/Cross-references: UNIPROT:P19850
 C/Superfamily: substance P precursor
 C/Keywords: amidated carboxyl end; tachykinin
 F/11/Modified site: amidated carboxyl end (Met) #status predicted

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 Db 8 FGLM 11

RESULT 4
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 probable substance P - smaller spotted catshark
 C/Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S33300
 R/Waugh, D.; Wang, Y.; Hazon, N.; Balmont, R.J.; Conlon, J.M.
 Eur. J. Biochem. 214, 469-474, 1993
 A/Title: Primary structures and biological activities of substance-P-related peptides fr
 A/Reference number: S33300; MUID:93392508; PMID:7685693
 A/Accession: S33300
 A/Molecule type: protein

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OM protein - protein search, using bw model

Run on: October 26, 2005, 08:13:37 ; Search time 96.444 Seconds
(without alignments)
17.316 Million cell updates/sec

Title: US-10-053-669-2

Perfect score: 21
Sequence: 1 FCIM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 250346

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	21	100.0	4	14	US-10-053-669-2
4	21	100.0	4	16	US-10-695-536-3
5	21	100.0	4	16	US-10-805-881-2
6	21	100.0	4	17	US-10-497-628-2
7	21	100.0	4	19	US-11-018-690-3
8	21	100.0	4	20	US-11-066-697-623
9	21	100.0	5	9	US-09-265-690C-1
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11	21	100.0	5	15	US-10-134-187-3

12	21	100.0	5	16	US-10-688-741-3	Sequence 3, Appli
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ALIGNMENTS

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; Publication No. US20010051345A1
; GENERAL INFORMATION:
; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-2

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; Sequence 3, Application US/10230133
; Publication No. US20030040625A1
; GENERAL INFORMATION:
; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; FILE REFERENCE: 2892-106
; CURRENT APPLICATION NUMBER: US/10/230,133
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 09/635,166
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4
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; Publication No. US20030077658A1
; GENERAL INFORMATION:
; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: N1427-005

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OM protein - protein search, using sw model

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Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 125705

Minimum DB seq length: 0

Maximum DB-seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

1: Issued_Patents_AA.*
2: /cgn2_6/pdata/1/1aa/5A_COMB.pep.*
3: /cgn2_6/pdata/1/1aa/5B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	1 US-08-441-551-63	Sequence 63, Appl
2	21	100.0	4	1 US-08-303-362A-63	Sequence 63, Appl
3	21	100.0	4	1 US-09-265-690C-2	Sequence 2, Appl
4	21	100.0	4	4 US-09-635-266-3	Sequence 3, Appl
5	21	100.0	4	4 US-10-230-133-3	Sequence 3, Appl
6	21	100.0	4	5 PCT-US95-05600-80	Sequence 80, Appl
7	21	100.0	5	1 US-07-934-553-2	Sequence 2, Appl
8	21	100.0	5	1 US-08-225-474-2	Sequence 2, Appl
9	21	100.0	5	2 US-08-070-301-6	Sequence 6, Appl
10	21	100.0	5	2 US-07-737-371E-6	Sequence 6, Appl
11	21	100.0	5	3 US-07-737-371E-48	Sequence 48, Appl
12	21	100.0	5	2 US-09-265-690C-1	Sequence 1, Appl
13	21	100.0	6	1 US-07-934-553-3	Sequence 3, Appl
14	21	100.0	6	1 US-08-225-474-3	Sequence 3, Appl
15	21	100.0	6	1 US-08-430-238-15	Sequence 15, Appl
16	21	100.0	6	2 US-07-737-371E-5	Sequence 5, Appl
17	21	100.0	6	3 US-09-317-125-5	Sequence 5, Appl
18	21	100.0	6	4 US-09-428-692-39	Sequence 39, Appl
19	21	100.0	6	4 US-09-428-692-41	Sequence 41, Appl
20	21	100.0	7	1 US-07-712-828B-7	Sequence 7, Appl
21	21	100.0	7	2 US-07-737-371E-8	Sequence 8, Appl
22	21	100.0	7	4 US-09-428-692-42	Sequence 42, Appl
23	21	100.0	8	2 US-07-737-371E-10	Sequence 10, Appl
24	21	100.0	8	2 US-07-737-371E-56	Sequence 56, Appl
25	21	100.0	9	1 US-08-346-849-6	Sequence 6, Appl
26	21	100.0	9	2 US-07-737-371E-60	Sequence 60, Appl
27	21	100.0	9	2 US-08-293-284A-6	Sequence 6, Appl

28	21	100.0	9	4 US-08-898-300-6	Sequence 6, Appl
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62	21	100.0	11	2 US-08-496-118-1	Sequence 1, Appl
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65	21	100.0	11	2 US-07-737-371E-16	Sequence 16, Appl
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81	21	100.0	11	4 US-09-570-022-1	Sequence 1, Appl
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128 16 76.2 5 4 US-10-337-105-4 Sequence 4, Appl1
129 16 76.2 6 3 US-09-196-93A-19 Sequence 19, Appl1
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132 16 76.2 7 1 US-08-286-262-3 Sequence 3, Appl1
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134 16 76.2 7 2 US-08-548-974-12 Sequence 12, Appl1
135 16 76.2 7 4 US-09-830-428A-21 Sequence 21, Appl1
136 16 76.2 7 4 US-09-274-454-12 Sequence 12, Appl1
137 16 76.2 7 4 US-09-672-865-2 Sequence 2, Appl1
138 16 76.2 8 1 US-08-522-326-4 Sequence 4, Appl1
139 16 76.2 8 1 US-08-522-326-9 Sequence 9, Appl1
140 16 76.2 8 1 US-08-522-326-10 Sequence 10, Appl1
141 16 76.2 8 1 US-08-522-326-14 Sequence 14, Appl1
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144 16 76.2 8 2 US-08-714-053-7 Sequence 7, Appl1
145 16 76.2 8 2 US-08-480-793-11 Sequence 11, Appl1
146 16 76.2 8 3 US-09-420-211-12 Sequence 12, Appl1
147 16 76.2 8 4 US-09-461-325-359 Sequence 359, Appl1
148 16 76.2 8 4 US-10-012-542-359 Sequence 359, Appl1
149 16 76.2 8 4 US-09-830-428A-14 Sequence 14, Appl1
150 16 76.2 8 4 US-09-586-106D-181 Sequence 181, Appl1

ALIGNMENTS

RESULT 1
US-08-441-591-63
Sequence 63, Application US/08441591
Patent No. 5637682
GENERAL INFORMATION:
APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO THE TACHYKININ
TITLE OF INVENTION: SUBSTANCE P
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,591
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/303,362
FILING DATE: 9-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-441-591-63
Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FGLM 4
Db 1 FGLM 4

RESULT 2
US-08-303-362A-63
Sequence 63, Application US/08303362A
Patent No. 5648214
GENERAL INFORMATION:
APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO THE TACHYKININ
TITLE OF INVENTION: SUBSTANCE P
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: October 26, 2005, 08:08:06 ; Search time 106.667 Seconds

(without alignments)
14,504 Million cell updates/sec

Title: ~~US-10-053-669-2~~

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 494136

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : ~~A:geneseq_16Dec04:*~~

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003ae:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	21	100.0	4	2	AAV31075 Non-cross
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4	21	100.0	4	3	AAV67577 P antagon
5	21	100.0	4	4	AAW91447 Tachykini
6	21	100.0	4	5	AAW10091 Substance
7	21	100.0	4	5	AAU77846 Tachykini
8	21	100.0	4	7	ADBE94198 High acti
9	21	100.0	4	8	ADRA43772 Human mag
10	21	100.0	5	2	AAW33009 Alpha-sub
11	21	100.0	5	2	AAW33008 Alpha-sub
12	21	100.0	5	2	AAW33007 Alpha-sub
13	21	100.0	5	2	AAW33010 Alpha-sub
14	21	100.0	5	2	AAW54549 Cholecyst
15	21	100.0	5	2	AAW54551 Cholecyst
16	21	100.0	5	2	AAW54550 Cholecyst
17	21	100.0	5	2	AAW54548 Cholecyst
18	21	100.0	5	2	AAW41687 Tetrapept
19	21	100.0	5	2	AAW96643 Substance
20	21	100.0	5	2	AAW50325 Neutrophil
21	21	100.0	5	2	AAW92660 Human tac
22	21	100.0	5	2	AAW92702 Human tac
23	21	100.0	5	3	AAW32025 Human/rat
24	21	100.0	5	3	AAV67576 P antagon
25	21	100.0	5	4	AAW91428 Tachykini

26	21	100.0	5	4	AAW91389 Tachykini
27	21	100.0	5	5	AAW10090 Substance
28	21	100.0	5	5	AAW10089 Substance
29	21	100.0	5	5	AAW10088 Substance
30	21	100.0	5	5	AAW77845 Tachykini
31	21	100.0	5	7	AAW94205 High acti
32	21	100.0	5	7	AAW94203 High acti
33	21	100.0	5	7	AAW94204 High acti
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35	21	100.0	5	8	ADN95078 Mammalian
36	21	100.0	5	8	ADP93603 E. coli m
37	21	100.0	8	8	ADP43771 Human mag
38	21	100.0	6	1	AAW40519 Sequence
39	21	100.0	6	1	AAW50694 Sequence
40	21	100.0	6	1	AAW50632 Substance
41	21	100.0	6	1	AAW61486 Peptide h
42	21	100.0	6	2	AAW07893 Cyclicopept
43	21	100.0	6	2	AAW07899 Cyclicopept
44	21	100.0	6	2	AAW21959 Substance
45	21	100.0	6	2	AAW27690 Cyclic ta
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53	21	100.0	6	3	AAW67575 P antagon
54	21	100.0	6	3	AAW7917 Neurokinin
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64	21	100.0	6	4	AAW07303 Neurokinin
65	21	100.0	6	4	AAW68998 Neurokinin
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68	21	100.0	6	4	AAW67862 Neurokinin
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71	21	100.0	6	7	ADW84202 High acti
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81	21	100.0	7	4	AAW91420 Tachykini
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104	21	100.0	9	4	AAAB91369	AAAB91369	Tachykinin
105	21	100.0	9	4	AAAG99348	AAAG99348	Atypical
106	21	100.0	9	7	AAE38833	AAE38833	Membrane
107	21	100.0	9	7	ADF92528	ADF92528	Substance
108	21	100.0	9	8	ADPO04477	ADPO04477	Substance
109	21	100.0	9	8	ADNP95076	ADNP95076	Substance
110	21	100.0	9	8	ADN15335	ADN15335	Mammalian
111	21	100.0	10	1	AAPE5633	AAPE5633	Substance
112	21	100.0	10	2	AAAR21933	AAAR21933	Substance
113	21	100.0	10	2	AAAR65181	AAAR65181	S. cerevis
114	21	100.0	10	2	AAAG99684	AAAG99684	Substance
115	21	100.0	10	2	AAAY06939	AAAY06939	Substance
116	21	100.0	10	2	AAW92663	AAW92663	Human tag
117	21	100.0	10	4	AAAB66675	AAAB66675	Tachykinin
118	21	100.0	10	4	AAAB91445	AAAB91445	Tachykinin
119	21	100.0	10	4	AAAG99347	AAAG99347	Atypical
120	21	100.0	10	4	AAAG64746	AAAG64746	Substance
121	21	100.0	10	8	ADN12181	ADN12181	Amino acti
122	21	100.0	10	8	ADN27868	ADN27868	Trichomon
123	21	100.0	11	1	AAPE61480	AAPE61480	Sequence
124	21	100.0	11	1	AAAR80312	AAAR80312	Sequence
125	21	100.0	11	1	AAAR11854	AAAR11854	Undecapent
126	21	100.0	11	2	AAAR3162	AAAR3162	Staic ac
127	21	100.0	11	2	AAAR28442	AAAR28442	Substance
128	21	100.0	11	2	AAAR21969	AAAR21969	Cyclic su
129	21	100.0	11	2	AAAR21942	AAAR21942	Substance
130	21	100.0	11	2	AAAR21962	AAAR21962	Substance
131	21	100.0	11	2	AAAR21945	AAAR21945	Substance
132	21	100.0	11	2	AAAR21963	AAAR21963	Substance
133	21	100.0	11	2	AAAR21949	AAAR21949	Substance
134	21	100.0	11	2	AAAR21951	AAAR21951	Substance
135	21	100.0	11	2	AAAR21934	AAAR21934	Substance
136	21	100.0	11	2	AAAR21946	AAAR21946	Substance
137	21	100.0	11	2	AAAR21964	AAAR21964	Substance
138	21	100.0	11	2	AAAR21970	AAAR21970	Cyclic su
139	21	100.0	11	2	AAAR21938	AAAR21938	Substance
140	21	100.0	11	2	AAAR21941	AAAR21941	Substance
141	21	100.0	11	2	AAAR21943	AAAR21943	Substance
142	21	100.0	11	2	AAAR21954	AAAR21954	Substance
143	21	100.0	11	2	AAAR42646	AAAR42646	Neurokini
144	21	100.0	11	2	AAAR85243	AAAR85243	Substance
145	21	100.0	11	2	AAAR77310	AAAR77310	Substance
146	21	100.0	11	2	AAAW33181	AAAW33181	Mono-DTPA
147	21	100.0	11	2	AAAW33180	AAAW33180	Mono-DTPA
148	21	100.0	11	2	AAAW04616	AAAW04616	Substance
149	21	100.0	11	2	AAAW97975	AAAW97975	Substance
150	21	100.0	11	2	AAAW42973	AAAW42973	Substrate

ALIGNMENTS

RESULT 1	
AAW41683	
ID	AAW41683 standard; peptide; 4 AA.
XX	
AC	AAW41683;
XX	
DT	09-JUN-1998 (first entry)
XX	
DE	Peptide used in ophthalmic drug to treat corneal disorders.
XX	
KW	Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye;
KW	keratitis; insulin like growth factor-I; IGF-I; eye drop.
XX	
OS	Synthetic.
XX	
PH	
Key	Location/Qualifiers

FT Modified-site 4 /note= "C-terminal amide"
 FT XX
 FN WO9749419-A1.
 PD 31-DEC-1997.
 PF 11-JUN-1997; 97WO-JP002015.
 PR 26-JUN-1996; 96JP-00165612.
 PA (SANTEN) SANTEN PHARM CO LTD.
 PI Nishida T, Nakamura M, Nakata K;
 DR WPI; 1998-076907/07.
 PT Ophthalmic drug composition containing tetra:peptide - is useful as
 PT corneal disorder remedy for corneal ulcer, corneal epithelial peeling,
 PT dry eye, keratitis.
 PS Claim 1; Page 15; 19pp; Japanese.
 XX
 CC The present sequence represents a tetrapeptide which is the active
 CC ingredient in an ophthalmic drug composition. It is used, together with
 CC insulin like growth factor-I (IGF-I), to treat corneal disorders such as
 CC corneal ulcer, corneal epithelial peeling, dry eye and keratitis. The
 CC dosage is 0.1-5000 (preferably 1-1000) mg/day of the tetrapeptide and
 CC 0.001-100 (preferably 0.01-10) mg/day of IGF-I. The preferable form of
 CC the composition is eye drops
 XX
 XQ Sequence 4 AA;

	Query Match	100.0%;	Score 21;	DB 2;	Length 4;
	Best Local Similarity	100.0%;	Pred. No.	1.8e+06;	
Matches	4;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
OY	1 FGLM 4				
Db	1 FGLM 4				
RESULT 2					
AAY31075					
ID AAY31075	standard; peptide; 4 AA.				
XX					
AC	AAY31075;				
XX					
D7	21-OCT-1999 (first entry)				
XX					
DE	Non-crosslinked protein particle peptide 124.				
XX					
KW	Non-crosslinked protein particle; diagnostic; therapy; monodisperse;				
XX	albumin; haemoglobin; nanometer; micrometer; clearance.				
OS	Synthetic.				
XX					
FH	Key	Location/Qualifiers			
FT	Modified-site	4			
FT		/note= "C-terminal amide"			
XX					
FN	US5945033-A.				
PD					
PD	31-AUG-1999.				
XX					
PF	12-NOV-1996;	96US-00747137.			
XX					
PR	15-JAN-1991;	91US-00641720.			
PR	13-OCT-1992;	92US-00959560.			
PR	01-JUN-1993;	93US-00069831.			
PR	14-MAR-1994;	94US-00212546.			
PA	(HEMO-) HEMOSPHERE INC.				

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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:36:48 ; Search time 170 Seconds

(without alignments)
15.061 Million cell updates/sec

Title: US-10-053-669-4
Perfect score: 22
Sequence: 1 FXGLM 5

Scoring table: BLOSUM62DX
Gapop-10.0 ; Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 150 summaries

Database :

1: uniprot_03:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	10	1	TKN1_SCYCA
2	22	100.0	10	1	TKNB_CHICK
3	22	100.0	10	1	TKNB_ONCMY
4	22	100.0	10	1	TKNB_RANCA
5	22	100.0	10	1	TKNB_RANCA
6	22	100.0	10	1	TKNC_RANCA
7	22	100.0	10	1	TKNC_PIG
8	22	100.0	10	1	TKNK_RANRI
9	22	100.0	10	1	TKN_BHARI
10	22	100.0	10	1	TKSI_AEDAE
11	22	100.0	10	1	TKS2_AEDAE
12	22	100.0	10	1	TKN1_PSEGU
13	22	100.0	10	1	TKN1_PSEGU
14	22	100.0	10	1	TKN1_PSEGU
15	22	100.0	10	1	TKN2_PSEGU
16	22	100.0	10	1	TKN2_PSEGU
17	22	100.0	10	1	TKN3_PSEGU
18	22	100.0	10	1	TKN4_PSEGU
19	22	100.0	10	1	TKN5_PSEGU
20	22	100.0	10	1	TKNA_CAYPO
21	22	100.0	10	1	TKNA_CHICK
22	22	100.0	10	1	TKNA_GADMO
23	22	100.0	10	1	TKNA_HORSE
24	22	100.0	10	1	TKNA_ONCMY
25	22	100.0	10	1	TKNA_RANCA
26	22	100.0	10	1	TKNA_RANCA
27	22	100.0	10	1	TKNA_SCYCA
28	22	100.0	10	1	TKN_ELECT
29	22	100.0	10	1	TKN_ELEMO
30	22	100.0	10	1	TKN_PHYFU
31	22	100.0	10	2	Q9UAR8

32	22	100.0	12	1	TKN1_KASMA	P08613 kassina mac
33	22	100.0	12	1	TKN_KASSE	P08611 kassina sen
34	22	100.0	13	1	CPI_APLCA	Q10398 aplysia cal
35	22	100.0	14	1	TKNM_RANMA	P40951 rana margar
36	22	100.0	16	1	TKN1_TORMA	Q71448 torpedo mar
37	22	100.0	18	1	TKN2_SCYCA	P08609 scyllorhinu
38	22	100.0	21	1	TKNC_CARAU	P25421 carassius a
39	22	100.0	21	2	Q9PRZ3	Q9PRZ3 oncorhynch
40	22	100.0	21	2	Q9PSJ1	Q9PSJ1 alligator m
41	22	100.0	24	2	Q9PRP3	Q9PRP3 sphyryna lew
42	22	100.0	29	2	Q673E3	Q673E3 dehalococco
43	22	100.0	33	2	Q8U5P2	Q8U5P2 agrobacteri
44	22	100.0	35	2	Q7UR55	Q7UR55 rhodospirell
45	22	100.0	39	2	Q832E2	Q832E2 enterococcu
46	22	100.0	42	2	Q62FX0	Q62FX0 burkholderi
47	22	100.0	44	2	Q9DDN3	Q9DDN3 xenopus lae
48	22	100.0	45	2	Q6LD93	Q6LD93 ractus sp.
49	22	100.0	48	2	Q9R820	Q9R820 escherichia
50	22	100.0	50	2	Q9AZN0	Q9AZN0 bacterioph
51	22	100.0	50	2	Q9CIA1	Q9CIA1 iactococcus
52	22	100.0	54	2	Q9PGV0	Q9PGV0 xylella fas
53	22	100.0	58	2	Q89H08	Q89H08 bradyrhizob
54	22	100.0	59	2	Q6KCL7	Q6KCL7 bacterioph
55	22	100.0	61	2	Q9TS58	Q9TS58 bos taurus
56	22	100.0	61	2	Q6MD93	Q6MD93 paracchlamyd
57	22	100.0	61	2	Q89463	Q89463 heliothis a
58	22	100.0	63	2	Q884T4	Q884T4 pseudomonas
59	22	100.0	65	2	Q7RZK1	Q7RZK1 neurospora
60	22	100.0	67	2	Q19443	Q19443 caenorhabdi
61	22	100.0	69	1	YAT1_RHOBL	P05443 rhodopseudo
62	22	100.0	69	2	Q9CJ49	Q9CJ49 iactococcus
63	22	100.0	69	2	Q6ME20	Q6ME20 paracchlamyd
64	22	100.0	69	2	Q8JXW0	Q8JXW0 virus pbich
65	22	100.0	70	2	Q94JCS	Q94JCS oryza sativ
66	22	100.0	70	2	Q8XWK6	Q8XWK6 ralsontia s
67	22	100.0	72	2	Q9Y494	Q9Y494 homo sapien
68	22	100.0	74	2	Q81WZ7	Q81WZ7 homo sapien
69	22	100.0	76	2	Q86JUN6	Q86JUN6 homo sapien
70	22	100.0	76	2	Q632P9	Q632P9 bacillus ce
71	22	100.0	76	2	Q72X55	Q72X55 bacillus ce
72	22	100.0	76	2	Q81KF4	Q81KF4 bacillus an
73	22	100.0	78	2	Q6HC90	Q6HC90 bacillus th
74	22	100.0	78	2	Q20445	Q20445 limulus pol
75	22	100.0	79	2	Q35733	Q35733 ractus nov
76	22	100.0	80	2	Q931B7	Q931B7 staphylococ
77	22	100.0	82	2	Q6BEK5	Q6BEK5 cryotolagus
78	22	100.0	82	2	Q98SD3	Q98SD3 guillardi
79	22	100.0	84	2	ATPL_THIFE	P41173 thicobacillu
80	22	100.0	84	2	Q6YME5	Q6YME5 caccopsylla
81	22	100.0	84	2	Q6YME9	Q6YME9 arycinnis b
82	22	100.0	84	2	Q6YME1	Q6YME1 arycinnis g
83	22	100.0	84	2	Q6YME5	Q6YME5 arycinnis o
84	22	100.0	84	2	Q6YME7	Q6YME7 arycinnis c
85	22	100.0	84	2	Q6YMG1	Q6YMG1 arycinnis m
86	22	100.0	84	2	Q6YMG3	Q6YMG3 arycinnis f
87	22	100.0	84	2	Q6YMG5	Q6YMG5 arycinnis u
88	22	100.0	84	2	Q6YMG7	Q6YMG7 arycinnis n
89	22	100.0	84	2	Q6YMK3	Q6YMK3 arycinnis m
90	22	100.0	84	2	Q6YMK7	Q6YMK7 arycinnis m
91	22	100.0	84	2	Q6YMK9	Q6YMK9 arycinnis m
92	22	100.0	84	2	Q6YML9	Q6YML9 arycinnis d
93	22	100.0	84	2	Q6YML1	Q6YML1 arycinnis d
94	22	100.0	84	2	Q6YML3	Q6YML3 arycinnis d
95	22	100.0	84	2	Q6YML5	Q6YML5 arycinnis d
96	22	100.0	84	2	Q6YML7	Q6YML7 arycinnis d
97	22	100.0	84	2	Q6YML9	Q6YML9 arycinnis d
98	22	100.0	84	2	Q6YML1	Q6YML1 arycinnis d
99	22	100.0	84	2	Q6YML3	Q6YML3 arycinnis d
100	22	100.0	84	2	Q6YML5	Q6YML5 arycinnis d
101	22	100.0	84	2	Q6YML7	Q6YML7 arycinnis d
102	22	100.0	84	2	Q6YML9	Q6YML9 arycinnis d
103	22	100.0	84	2	Q6YML1	Q6YML1 arycinnis d
104	22	100.0	84	2	Q6YML3	Q6YML3 arycinnis d

105	22	100.0	87	2	Q86U07	Q86U07 homo sapien
106	22	100.0	87	2	Q6YMB9	Q6YMB9 livilla com
107	22	100.0	87	2	Q6YMC1	Q6YMC1 livilla bae
108	22	100.0	87	2	Q6YMC3	Q6YMC3 livilla cap
109	22	100.0	87	2	Q6YMC9	Q6YMC9 livilla mon
110	22	100.0	87	2	Q6YMD1	Q6YMD1 livilla mon
111	22	100.0	87	2	Q6YMD3	Q6YMD3 livilla mon
112	22	100.0	87	2	Q6YMD5	Q6YMD5 livilla mau
113	22	100.0	87	2	Q6YMD7	Q6YMD7 livilla bla
114	22	100.0	87	2	Q6YMD9	Q6YMD9 livilla adu
115	22	100.0	87	2	Q6YME1	Q6YME1 cyamophila
116	22	100.0	87	2	Q6YME3	Q6YME3 cacopsylla
117	22	100.0	87	2	Q6YME5	Q6YME5 arctimilis o
118	22	100.0	87	2	Q6YMG7	Q6YMG7 arctainilla
119	22	100.0	87	2	Q6YMH5	Q6YMH5 arctainilla
120	22	100.0	87	2	Q6YMI3	Q6YMI3 arctainilla
121	22	100.0	87	2	Q6YMA9	Q6YMA9 arctimilis n
122	22	100.0	87	2	Q6YMA1	Q6YMA1 arctainilla
123	22	100.0	87	2	Q6YMA5	Q6YMA5 arctaina vi
124	22	100.0	87	2	Q6YMA7	Q6YMA7 arctaina nu
125	22	100.0	87	2	Q6YMQ3	Q6YMQ3 arctaina ad
126	22	100.0	87	2	Q6YMQ7	Q6YMQ7 arctaina ad
127	22	100.0	87	2	Q6YMO9	Q6YMO9 acizzia unc
128	22	100.0	87	2	Q6YMR1	Q6YMR1 acizzia hol
129	22	100.0	87	2	Q75Y73	Q75Y73 euhadra qua
130	22	100.0	89	2	Q8LMB5	Q8LMB5 oryza saativ
131	22	100.0	92	1	TKN2_OCTVU	Q81682 octopus vul
132	22	100.0	92	2	Q6AL16	Q6AL16 desulfoacte
133	22	100.0	93	1	Y011_MYCBO	P67377 mycobacteri
134	22	100.0	93	1	Y011_MYCTU	P67376 mycobacteri
135	22	100.0	93	1	Y013_MYCLE	Q9J267 mycobacteri
136	22	100.0	93	2	Q6J2W7	Q6J2W7 boletellu
137	22	100.0	93	2	Q744R9	Q744R9 mycobacteri
138	22	100.0	94	2	Q82P05	Q82P05 streptomyce
139	22	100.0	95	2	Q9Y6T4	Q9Y6T4 homo sapien
140	22	100.0	96	1	YNBC_ECO57	P64462 escherichia
141	22	100.0	96	1	YNBC_ECOLI	P64461 escherichia
142	22	100.0	96	2	Q86U08	Q86U08 homo sapien
143	22	100.0	96	2	Q66E24	Q66E24 yerisnla ps
144	22	100.0	96	2	Q74PW0	Q74PW0 yerisnla pe
145	22	100.0	96	2	Q82IT1	Q82IT1 yerisnla pe
146	22	100.0	96	2	Q83L16	Q83L16 shigella fl
147	22	100.0	97	2	Q8ND57	Q8ND57 homo sapien
148	22	100.0	97	2	Q6AB45	Q6AB45 propionibac
149	22	100.0	98	2	Q7YCY0	Q7YCY0 sarcophaga
150	22	100.0	99	2	Q9MLP9	Q9MLP9 limulus pol

ALIGNMENTS

RESULT 1
TKN1_SCYCA STANDARD; PRT; 10 AA.
ID TKN1_SCYCA
AC P08608;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Scyllorhynchus I.
OS Scyllorhynchus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine; PubMed=2422058; DOI=10.1016/0014-5793(86)80521-X;
RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;
RT "Scyllorhynchus I and II: two novel tachykinins from dogfish gut.";
RL FEBS Lett. 200:111-116(1986).
RN [2]
RP SEQUENCE.

RC TISSUE=Brain; PubMed=7685693;
RX MEDLINE=93292508; Balmert R.J., Conlon J.M.;
RA Maugh D., Wang Y., Hazon N., Balmert R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
RT peptides from the brain of the dogfish, Scyllorhynchus canicula.";
RL Eur. J. Biochem. 214:469-474(1993).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A24867; A24867.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ, 1.
KW Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.
FT MOD_RES 10 Methionine amide.
SQ SEQUENCE 10 AA; 1219 MW; D0602D6B59C33AA9 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 10;
Best Local Similarity 80.0%; Pred.No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGLM 5
|:|:|
Db 6 FXGLM 10

RESULT 2
TKNB_CHICK STANDARD; PRT; 10 AA.
ID TKNB_CHICK
AC P19851;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neurokinin A (Substance K) (Neuromedin L).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=88204263; PubMed=2452461; DOI=10.1016/0167-0115(88)90050-X;
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT "Arg3]substance P and neurokinin A from chicken small intestine.";
RL Regul. Pept. 20:171-180(1988).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR; UN0024; UN0024.
DR PDB; 1NET; NMR; A=1-10.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin, 1.
DR PROSITE; PS00267; TACHYKININ, 1.
KW 3D-structure; Amidation; Direct protein sequencing; Neuropeptide;
KW Tachykinin.
FT MOD_RES 10 Methionine amide.
SQ SEQUENCE 10 AA; 1134 MW; 8A6BA062C9D5BAB1 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 10;
Best Local Similarity 80.0%; Pred.No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGLM 5
|:|:|
Db 6 FXGLM 10

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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:37:28 ; Search time 39 Seconds
(without alignments)
12.335 Million cell updates/sec

Title: US-10-053-669-4
Perfect score: 22
Sequence: 1 FXGLM 5

Scoring table: BLOSUM62DX
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :
1: PIR 79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	10	1 SPBGK	neurokinin K - pig
2	22	100.0	10	2 JN0024	neurokinin A - chi
3	22	100.0	10	2 B49581	neurokinin II - ye
4	22	100.0	10	2 A49581	neurokinin I - ye
5	22	100.0	10	2 A24867	neurokinin I - s
6	22	100.0	10	2 S23307	neurokinin A - ral
7	22	100.0	10	2 S23186	neurokinin A - Acl
8	22	100.0	10	2 S07202	neurokinin A - tw
9	22	100.0	10	2 C61033	neurokinin C -
10	22	100.0	10	2 B61033	neurokinin B -
11	22	100.0	10	2 S27178	neurokinin A-relat
12	22	100.0	11	1 A60654	neurokinin P - qu
13	22	100.0	11	1 E00C	neurokinin P - musk
14	22	100.0	11	1 E00C	neurokinin P - musk
15	22	100.0	11	1 E00C	neurokinin P - musk
16	22	100.0	11	1 E00C	neurokinin P - musk
17	22	100.0	11	2 JN0023	neurokinin P - chic
18	22	100.0	11	2 S33300	neurokinin P - chic
19	22	100.0	11	2 S07203	neurokinin P - chic
20	22	100.0	11	2 C60409	neurokinin P - chic
21	22	100.0	11	2 B60409	neurokinin P - chic
22	22	100.0	11	2 D60409	neurokinin P - chic
23	22	100.0	11	2 S23308	neurokinin P - chic
24	22	100.0	11	2 S23306	neurokinin P - chic
25	22	100.0	11	2 S07201	neurokinin P - chic
26	22	100.0	11	2 A61033	neurokinin P - chic
27	22	100.0	11	2 S10059	neurokinin P - chic
28	22	100.0	12	2 S07206	neurokinin P - chic
29	22	100.0	12	2 S07206	neurokinin P - chic

30	22	100.0	16	2 A60839	neurokinin A homo
31	22	100.0	18	2 B24867	neurokinin II -
32	22	100.0	21	2 JH0361	neurokinin I -
33	22	100.0	33	2 F97371	neurokinin I -
34	22	100.0	50	2 A86583	neurokinin I -
35	22	100.0	54	2 C82836	neurokinin I -
36	22	100.0	63	2 TC2412	neurokinin I -
37	22	100.0	67	2 T16071	neurokinin I -
38	22	100.0	69	2 E86644	neurokinin I -
39	22	100.0	69	2 S04666	neurokinin I -
40	22	100.0	72	2 JC5455	neurokinin I -
41	22	100.0	72	2 T62742	neurokinin I -
42	22	100.0	80	2 S13840	neurokinin I -
43	22	100.0	82	2 E90119	neurokinin I -
44	22	100.0	93	2 E86910	neurokinin I -
45	22	100.0	93	2 A70659	neurokinin I -
46	22	100.0	96	2 E90894	neurokinin I -
47	22	100.0	96	2 D85723	neurokinin I -
48	22	100.0	96	2 AF0050	neurokinin I -
49	22	100.0	96	2 A64906	neurokinin I -
50	22	100.0	97	2 S12958	neurokinin I -
51	22	100.0	99	2 S14586	neurokinin I -
52	22	100.0	102	2 F90997	neurokinin I -
53	22	100.0	102	2 E86817	neurokinin I -
54	22	100.0	102	2 T17741	neurokinin I -
55	22	100.0	102	2 AB0101	neurokinin I -
56	22	100.0	103	2 S28823	neurokinin I -
57	22	100.0	103	2 D49852	neurokinin I -
58	22	100.0	104	2 F87731	neurokinin I -
59	22	100.0	105	2 JE0384	neurokinin I -
60	22	100.0	109	2 AF0940	neurokinin I -
61	22	100.0	112	1 SPRTA	neurokinin I -
62	22	100.0	115	1 SPRTA	neurokinin I -
63	22	100.0	115	1 SPRTA	neurokinin I -
64	22	100.0	116	2 T65342	neurokinin I -
65	22	100.0	116	2 A43779	neurokinin I -
66	22	100.0	116	2 C72232	neurokinin I -
67	22	100.0	118	1 IECC5B	neurokinin I -
68	22	100.0	121	2 C42573	neurokinin I -
69	22	100.0	122	2 T09187	neurokinin I -
70	22	100.0	123	2 B69050	neurokinin I -
71	22	100.0	124	2 B86771	neurokinin I -
72	22	100.0	126	2 T63117	neurokinin I -
73	22	100.0	126	2 A25905	neurokinin I -
74	22	100.0	129	1 SPRTB	neurokinin I -
75	22	100.0	130	1 SPRTB	neurokinin I -
76	22	100.0	130	1 SPRTB	neurokinin I -
77	22	100.0	130	2 S47038	neurokinin I -
78	22	100.0	130	2 A52526	neurokinin I -
79	22	100.0	131	2 A53024	neurokinin I -
80	22	100.0	131	2 B89869	neurokinin I -
81	22	100.0	133	2 T17787	neurokinin I -
82	22	100.0	135	2 AG2021	neurokinin I -
83	22	100.0	136	2 F97328	neurokinin I -
84	22	100.0	137	2 F97328	neurokinin I -
85	22	100.0	145	2 S76409	neurokinin I -
86	22	100.0	154	2 B71046	neurokinin I -
87	22	100.0	159	2 A39624	neurokinin I -
88	22	100.0	161	2 J02402	neurokinin I -
89	22	100.0	161	2 S08206	neurokinin I -
90	22	100.0	163	2 H97417	neurokinin I -
91	22	100.0	163	2 AG1931	neurokinin I -
92	22	100.0	166	2 DEMS6	neurokinin I -
93	22	100.0	172	1 DEMS6	neurokinin I -
94	22	100.0	172	1 DEMS6	neurokinin I -
95	22	100.0	173	2 T11348	neurokinin I -
96	22	100.0	173	2 E83931	neurokinin I -
97	22	100.0	173	2 S65999	neurokinin I -
98	22	100.0	174	2 T11491	neurokinin I -
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100	22	100.0	174	2 D82629	neurokinin I -
101	22	100.0	175	1 DEB06	neurokinin I -
102	22	100.0	175	2 T11504	neurokinin I -

103	22	100.0	175	2	T11452	NADH2 dehydrogenas
104	22	100.0	175	2	T11451	NADH2 dehydrogenas
105	22	100.0	175	2	T11453	NADH2 dehydrogenas
106	22	100.0	175	2	S41846	NADH2 dehydrogenas
107	22	100.0	175	2	S26162	NADH2 dehydrogenas
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109	22	100.0	175	2	S41831	NADH2 dehydrogenas
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115	22	100.0	176	2	S02210	con-8 protein - Ne
116	22	100.0	178	2	T48711	hypothetical prote
117	22	100.0	180	2	F87358	hypothetical prote
118	22	100.0	181	2	F81851	hypothetical prote
119	22	100.0	184	2	S74741	hypothetical prote
120	22	100.0	184	2	E90077	conserved hypotet
121	22	100.0	187	2	T02887	probable calmodul
122	22	100.0	187	2	AF3009	hypothetical prote
123	22	100.0	191	2	AE2135	hypothetical prote
124	22	100.0	193	2	T26510	hypothetical prote
125	22	100.0	195	2	H98274	hypothetical prote
126	22	100.0	197	2	T36696	probable regulator
127	22	100.0	198	2	AF1870	hypothetical prote
128	22	100.0	199	2	S73702	hypothetical prote
129	22	100.0	200	1	A39741	cytochrome c bioge
130	22	100.0	203	2	B90055	hypothetical prote
131	22	100.0	205	2	T08398	calmodulin homolo
132	22	100.0	208	2	T08452	hypothetical prote
133	22	100.0	210	2	D97502	hypothetical prote
134	22	100.0	210	2	AH2720	RhtB family transp
135	22	100.0	210	2	T28002	hypothetical prote
136	22	100.0	210	2	AD2818	conserved hypotet
137	22	100.0	211	1	TCMS6	interleukin-6 prec
138	22	100.0	211	2	A34247	interleukin-6 prec
139	22	100.0	211	2	D69529	conserved hypotet
140	22	100.0	215	2	JX0244	pyroglutamy1-pept
141	22	100.0	215	2	S23432	two component resp
142	22	100.0	216	2	A12635	prostaglandin B2 r
143	22	100.0	217	2	D53116	conserved hypotet
144	22	100.0	219	2	F69341	serine acetyltrans
145	22	100.0	220	2	D72349	conserved hypotet
146	22	100.0	223	2	D82210	conserved hypotet
147	22	100.0	223	2	E90392	hypothetical prote
148	22	100.0	228	2	E86253	hypothetical prote
149	22	100.0	229	2	E71010	hypothetical prote
150	22	100.0	230	1	H64634	conserved hypotet

ALIGNMENTS

RESULT 1
SPGSK
neuromedin K - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
C/Accession: A01560
R/Kangawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.
Biochem. Biophys. Res. Commun. 114, 533-540, 1983
A/Title: Neuromedin K: a novel mammalian tachykinin identified in porcine spinal cord.
A/Reference number: A01560; PMID:83282812; PMID:6576785
A/Accession: A01560
A/Molecule type: protein
A/Residues: 1-10 <KAN>
A/Cross-references: UNIPROT:P01292
A/Note: the structure of the peptide was confirmed by synthesis
C/Comment: The biological source of this peptide is spinal cord. It stimulates smooth mu
C/Superfamily: neurokinin B precursor
C/Keywords: amidated carboxyl end; hormone; spinal cord
P/10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 22; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGLM 5
|:|:|
Db 6 FVGLM 10

RESULT 2
JN0024
neurokinin A - chicken
C/Species: Gallus gallus (chicken)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: JN0024
R/Conlon, J.M.; Karsouls, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A/Title: [Arg3]substance P and neurokinin A from chicken small intestine.
A/Reference number: JN0023; PMID:88204263; PMID:2452461
A/Accession: JN0024
A/Molecule type: protein
A/Residues: 1-10 <CON>
A/Cross-references: UNIPROT:P19851
C/Superfamily: substance P precursor
C/Keywords: amidated carboxyl end; neuropeptide; tachykinin
P/10/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 22; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGLM 5
|:|:|
Db 6 FVGLM 10

RESULT 3
B49581
sialokinin II - yellow fever mosquito
C/Species: Aedes aegypti (yellow fever mosquito)
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C/Accession: B49581
R/Champagne, D.E.; Ribeiro, J.M.
Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994
A/Title: Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito Aek
A/Reference number: A49581; PMID:94105119; PMID:8278354
A/Accession: B49581
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <CHA>
A/Cross-references: UNIPROT:P42635
A/Experimental source: Rockefeller, salivary gland
A/Note: sequence extracted from NCBI backbone (NCBIP:141842)

Query Match 100.0%; Score 22; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGLM 5
|:|:|
Db 6 FVGLM 10

RESULT 4
A49581
sialokinin I - yellow fever mosquito
C/Species: Aedes aegypti (yellow fever mosquito)
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A49581
R/Champagne, D.E.; Ribeiro, J.M.
Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994
A/Title: Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito Aek
A/Reference number: A49581; PMID:94105119; PMID:8278354

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:40:49 ; Search time 166 Seconds
(without alignments)
12.576 Million cell updates/sec

Title: US-10-053-669-4
Perfect score: 1 FXGLM 5
Sequence: 1 FXGLM 5

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 150 summaries

Database: Published Applications AA*
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubppa/PCRUS_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep:*
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21: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	5	9	US-09-265-690C-1
2	22	100.0	5	9	US-09-265-690C-4
3	22	100.0	5	14	US-10-230-133-4
4	22	100.0	5	14	US-10-053-669-1
5	22	100.0	5	22	US-10-053-669-4
6	22	100.0	5	15	US-10-134-187-3
7	22	100.0	5	16	US-10-688-741-3
8	22	100.0	5	16	US-10-695-536-4
9	22	100.0	5	16	US-10-805-881-1
10	22	100.0	5	16	US-10-805-881-4
11	22	100.0	5	16	US-10-720-039-3

12	22	100.0	5	17	US-10-497-628-15	Sequence 15, Appl
13	22	100.0	5	17	US-10-451-304-12	Sequence 12, Appl
14	22	100.0	5	19	US-11-018-690-4	Sequence 4, Appl
15	22	100.0	5	20	US-11-066-697-604	Sequence 604, App
16	22	100.0	5	20	US-11-025-494-3	Sequence 3, Appl
17	22	100.0	6	14	US-10-168-789A-38	Sequence 38, Appl
18	22	100.0	6	17	US-10-497-628-14	Sequence 14, Appl
19	22	100.0	6	20	US-11-066-697-5595	Sequence 595, App
20	22	100.0	6	20	US-11-066-697-5597	Sequence 597, App
21	22	100.0	6	20	US-11-066-697-601	Sequence 601, App
22	22	100.0	7	14	US-10-036-542-110	Sequence 110, App
23	22	100.0	7	14	US-10-036-542-111	Sequence 111, App
24	22	100.0	7	14	US-10-168-789A-37	Sequence 37, Appl
25	22	100.0	7	15	US-10-134-187-2	Sequence 2, Appl
26	22	100.0	7	15	US-10-688-741-2	Sequence 2, Appl
27	22	100.0	7	16	US-10-720-039-2	Sequence 13, Appl
28	22	100.0	7	17	US-10-497-628-13	Sequence 13, Appl
29	22	100.0	7	20	US-11-066-697-530	Sequence 530, App
30	22	100.0	7	20	US-11-066-697-556	Sequence 596, App
31	22	100.0	7	20	US-11-066-697-607	Sequence 607, App
32	22	100.0	8	9	US-09-910-552-36	Sequence 36, Appl
33	22	100.0	8	14	US-10-168-789A-36	Sequence 36, Appl
34	22	100.0	8	15	US-10-643-465-36	Sequence 36, Appl
35	22	100.0	8	17	US-10-497-628-12	Sequence 12, Appl
36	22	100.0	8	20	US-11-066-697-583	Sequence 583, App
37	22	100.0	8	20	US-11-066-697-592	Sequence 592, App
38	22	100.0	8	20	US-11-066-697-600	Sequence 600, App
39	22	100.0	9	14	US-10-036-542-112	Sequence 112, App
40	22	100.0	9	14	US-10-168-789A-35	Sequence 35, Appl
41	22	100.0	9	15	US-10-134-187-1	Sequence 1, Appl
42	22	100.0	9	15	US-10-688-741-1	Sequence 1, Appl
43	22	100.0	9	16	US-10-720-039-1	Sequence 1, Appl
44	22	100.0	9	20	US-11-066-697-545	Sequence 545, App
45	22	100.0	9	20	US-11-066-697-622	Sequence 622, App
46	22	100.0	9	20	US-11-025-494-1	Sequence 1, Appl
47	22	100.0	10	9	US-09-853-161-110	Sequence 110, App
48	22	100.0	10	9	US-09-852-699-110	Sequence 110, App
49	22	100.0	10	10	US-09-852-699-110	Sequence 110, App
50	22	100.0	10	10	US-09-988-792-11	Sequence 11, Appl
51	22	100.0	10	10	US-10-197-954-98	Sequence 98, Appl
52	22	100.0	10	14	US-10-197-954-99	Sequence 99, Appl
53	22	100.0	10	14	US-10-168-789A-34	Sequence 34, Appl
54	22	100.0	10	14	US-10-267-918-1	Sequence 2, Appl
55	22	100.0	10	14	US-10-058-993-110	Sequence 110, App
56	22	100.0	10	15	US-10-360-101-91	Sequence 91, Appl
57	22	100.0	10	15	US-10-445-400-1	Sequence 1, Appl
58	22	100.0	10	15	US-10-445-400-2	Sequence 2, Appl
59	22	100.0	10	17	US-10-718-071-6	Sequence 98, Appl
60	22	100.0	10	17	US-10-760-085-98	Sequence 98, Appl
61	22	100.0	10	17	US-10-760-085-99	Sequence 99, Appl
62	22	100.0	10	17	US-10-451-304-1	Sequence 1, Appl
63	22	100.0	10	17	US-10-451-304-2	Sequence 2, Appl
64	22	100.0	10	17	US-10-451-304-3	Sequence 3, Appl
65	22	100.0	10	18	US-10-994-170-1	Sequence 1, Appl
66	22	100.0	10	18	US-10-994-170-2	Sequence 2, Appl
67	22	100.0	10	18	US-10-951-993-110	Sequence 110, App
68	22	100.0	10	18	US-11-066-697-531	Sequence 531, App
69	22	100.0	10	20	US-11-066-697-532	Sequence 532, App
70	22	100.0	10	20	US-11-066-697-533	Sequence 533, App
71	22	100.0	10	20	US-11-066-697-544	Sequence 544, App
72	22	100.0	10	20	US-11-066-697-546	Sequence 546, App
73	22	100.0	10	20	US-11-066-697-559	Sequence 559, App
74	22	100.0	10	20	US-11-066-697-573	Sequence 573, App
75	22	100.0	10	20	US-11-066-697-574	Sequence 574, App
76	22	100.0	10	20	US-11-066-697-621	Sequence 621, App
77	22	100.0	10	20	US-11-079-147-71	Sequence 71, Appl
78	22	100.0	11	9	US-09-265-690C-3	Sequence 3, Appl
79	22	100.0	11	9	US-09-935-682-64	Sequence 64, Appl
80	22	100.0	11	9	US-09-841-0918-26	Sequence 26, Appl
81	22	100.0	11	10	US-09-988-792-1	Sequence 1, Appl
82	22	100.0	11	10	US-09-988-792-6	Sequence 6, Appl
83	22	100.0	11	10	US-09-988-792-7	Sequence 7, Appl
84	22	100.0	11	10	US-09-988-792-7	Sequence 7, Appl

85	22	100.0	11	10	US-09-988-792-8	Sequence 8, Appli
86	22	100.0	11	10	US-09-988-792-9	Sequence 9, Appli
87	22	100.0	11	10	US-09-988-792-10	Sequence 10, Appli
88	22	100.0	11	13	US-10-002-593-4	Sequence 4, Appli
89	22	100.0	11	14	US-10-230-133-1	Sequence 1, Appli
90	22	100.0	11	14	US-10-053-669-3	Sequence 3, Appli
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92	22	100.0	11	14	US-10-114-823B-24	Sequence 24, Appli
93	22	100.0	11	14	US-10-197-954-48	Sequence 48, Appli
94	22	100.0	11	14	US-10-197-954-117	Sequence 117, App
95	22	100.0	11	14	US-10-197-954-130	Sequence 130, App
96	22	100.0	11	14	US-10-197-954-138	Sequence 138, App
97	22	100.0	11	14	US-10-251-703-25	Sequence 25, Appli
98	22	100.0	11	14	US-10-168-789A-17	Sequence 17, Appli
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; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
US-09-265-690C-1

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Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB      1 FXGLM 5

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; Sequence 4, Application US/09265690C
; Publication No. US20010051345A1
; GENERAL INFORMATION:
; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265,690C
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: AMIDATION
; NAME/KEY: VARIANT
; LOCATION: (2)..(2)
; OTHER INFORMATION: "X" may be either Phe or Val.
US-09-265-690C-4

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Query Match          100.0%; Score 22; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 FXGLM 5

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; Sequence 4, Application US/10230133
; Publication No. US20030040625A1
; GENERAL INFORMATION:
; APPLICANT: Wellb, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and
; methods for treatment of abnormal physiological states

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 08:37:58 ; Search time 43 Seconds

(without alignments)
8.680 Million cell updates/sec

Title: US-10-053-669-4
Perfect score: 22
Sequence: 1 FXGLM 5

Scoring table: BLASTSUM62DX
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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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6	22	100.0	5	1	US-08-418-994-1
7	22	100.0	5	1	US-08-391-814-1
8	22	100.0	5	1	US-08-441-591-61
9	22	100.0	5	1	US-08-303-362A-61
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ALIGNMENTS

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 ; Patent No. 5304632
 ; GENERAL INFORMATION:
 ; APPLICANT: Vaudry, Hubert
 ; APPLICANT: Conlon, Michael J.
 ; TITLE OF INVENTION: Neuropeptides of the Tachykinin Family
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Zarley, McKee, Thomte, Voornhees, and Sease
 ; STREET: 801 Grand, Suite 3200
 ; CITY: Des Moines
 ; STATE: Iowa
 ; COUNTRY: United States
 ; ZIP: 50309
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/753, 909B
 ; FILING DATE: 19910903
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 9106759
 ; FILING DATE: 04-JUN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sease, Edmund J.
 ; REGISTRATION NUMBER: 24,741
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (515)-288-3667
 ; TELEFAX: (515)-288-1338
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: AMINO ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: C-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Rana ridibunda
 ; DEVELOPMENTAL STAGE: adult
 ; TISSUE TYPE: brain
 ; US-07-753-909B-3

Query Match 100.0%; Score 22; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
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 Db 1 FXGLM 5
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 US-07-934-553-2
 ; Sequence 2, Application US/07934553
 ; Patent No. 5314690
 ; GENERAL INFORMATION:
 ; APPLICANT: PATTERSON, ROY
 ; APPLICANT: HARRIS, KATHLEEN E
 ; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TILTON, FALLON, LUNGKUS & CHESTNUT
 ; STREET: 100 SOUTH WACKER DRIVE
 ; CITY: CHICAGO
 ; STATE: ILLINOIS
 ; COUNTRY: USA
 ; ZIP: 60606-4002
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/934, 553
 ; FILING DATE: 19920821
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/705, 071
 ; FILING DATE: 24-MAY-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FENTRESS, SUSAN B
 ; REGISTRATION NUMBER: 31,327
 ; REFERENCE/DOCKET NUMBER: NU-9033CIP
 ; TELECOMMUNICATION INFORMATION:

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: October 26, 2005, 08:34:00 ; Search time 165 Seconds

(without alignments)
11.720 Million cell updates/sec

Title: US-10-053-669-4

Perfect score: 22
Sequence: 1 FXGLM 5

Scoring table: BLOSUM62DX
Gapop 10.0, Gapext 0.5

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Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: geneeqp20008:.*
4: geneeqp20018:.*
5: geneeqp20028:.*
6: geneeqp20038:.*
7: geneeqp20048:.*
8: geneeqp20058:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	5	2 AAR33009	Aar33009 Alpha-sub
2	22	100.0	5	2 AAR33008	Aar33008 Alpha-sub
3	22	100.0	5	2 AAR33007	Aar33007 Alpha-sub
4	22	100.0	5	2 AAR33010	Aar33010 Alpha-sub
5	22	100.0	5	2 AAR60134	Aar60134 COOH-term
6	22	100.0	5	2 AAR54549	Aar54549 Cholecyt
7	22	100.0	5	2 AAR54551	Aar54551 Cholecyt
8	22	100.0	5	2 AAR54550	Aar54550 Cholecyt
9	22	100.0	5	2 AAR54548	Aar54548 Cholecyt
10	22	100.0	5	2 AAR41687	Aar41687 Tetrapt
11	22	100.0	5	2 AAR96643	Aar96643 Substance
12	22	100.0	5	2 AAY50325	Aay50325 Neutroph
13	22	100.0	5	2 AAW92660	Aaw92660 Human tac
14	22	100.0	5	3 AAB33028	Aab33028 Mammalian
15	22	100.0	5	3 AAB33025	Aab33025 Human/rat
16	22	100.0	5	3 AAT67576	Aat67576 P antag
17	22	100.0	5	4 AAB66674	Aab66674 C-term
18	22	100.0	5	4 AAB82430	Aab82430 Fluorinat
19	22	100.0	5	4 AAB82431	Aab82431 Fluorinat
20	22	100.0	5	4 AAB91428	Aab91428 Tachykin
21	22	100.0	5	4 AAB70556	Aab70556 Octopus t
22	22	100.0	5	5 AAB10088	Aab10088 Human dec
23	22	100.0	5	5 AAB10088	Aab10088 Substance
24	22	100.0	5	5 AAU77847	Aau77847 Tachykin
25	22	100.0	5	5 AAU77845	Aau77845 Tachykin

26	22	100.0	5	7 ADC64000	Adc64000 Tachykin
27	22	100.0	5	7 ADE94203	Ade94203 High acti
28	22	100.0	5	7 ADF92530	Adf92530 Substance
29	22	100.0	5	8 ADN12180	Adn12180 Tachykin
30	22	100.0	5	8 ADN95078	Adn95078 Mammalian
31	22	100.0	5	8 ADR43774	Adr43774 Mammalian
32	22	100.0	5	8 ADR43771	Adr43771 Human mag
33	22	100.0	6	1 AAP30443	Aap30443 Sequence
34	22	100.0	6	1 AAP40519	Aap40519 Sequence
35	22	100.0	6	1 AAP50694	Aap50694 Sequence
36	22	100.0	6	1 AAP50632	Aap50632 Substance
37	22	100.0	6	1 AAP61486	Aap61486 Peptide h
38	22	100.0	6	2 AAR07897	Aar07897 Cylopept
39	22	100.0	6	2 AAR07893	Aar07893 Cylopept
40	22	100.0	6	2 AAR21959	Aar21959 Substance
41	22	100.0	6	2 AAR27696	Aar27696 Cyclic ta
42	22	100.0	6	2 AAR27694	Aar27694 Cyclic ta
43	22	100.0	6	2 AAR27695	Aar27695 Cyclic ta
44	22	100.0	6	2 AAW9686	Aaw9686 Substance
45	22	100.0	6	2 AAW92706	Aaw92706 Human tac
46	22	100.0	6	2 AAW92659	Aaw92659 Human tac
47	22	100.0	6	2 AAY11052	Aay11052 Non-cross
48	22	100.0	6	3 AAT67575	Aat67575 P antag
49	22	100.0	6	4 AAB82453	Aab82453 Fluorinat
50	22	100.0	6	4 AAB82432	Aab82432 Fluorinat
51	22	100.0	6	4 AAB82436	Aab82436 Fluorinat
52	22	100.0	6	4 AAB82433	Aab82433 Fluorinat
53	22	100.0	6	4 AAB81421	Aab81421 Tachykin
54	22	100.0	6	4 AAB81425	Aab81425 Tachykin
55	22	100.0	6	4 AAB81419	Aab81419 Tachykin
56	22	100.0	6	4 AAG93351	Aag93351 Aclycal
57	22	100.0	6	4 AAB74306	Aab74306 Peptide a
58	22	100.0	6	4 AAB98884	Aab98884 Chimeric
59	22	100.0	6	4 AAB98886	Aab98886 Chimeric
60	22	100.0	6	5 AAB10087	Aab10087 Substance
61	22	100.0	6	5 AAB10086	Aab10086 Substance
62	22	100.0	6	6 AAB17288	Abj17288 Rhodopsin
63	22	100.0	7	1 ADE94202	Ade94202 High acti
64	22	100.0	7	1 AAP20310	Aap20310 Ty8-SP5-
65	22	100.0	7	2 AAR21956	Aar21956 Substance
66	22	100.0	7	2 AAR21957	Aar21957 Substance
67	22	100.0	7	2 AAW92539	Aaw92539 Aap-Ser-P
68	22	100.0	7	2 AAY50324	Aay50324 Neutroph
69	22	100.0	7	2 AAW92662	Aaw92662 Human tac
70	22	100.0	7	2 AAW92705	Aaw92705 Human tac
71	22	100.0	7	3 AAT67574	Aat67574 P antag
72	22	100.0	7	4 AAB80323	Aab80323 Human pro
73	22	100.0	7	4 AAB80324	Aab80324 Human pro
74	22	100.0	7	4 AAB82428	Aab82428 Fluorinat
75	22	100.0	7	4 AAB82429	Aab82429 Fluorinat
76	22	100.0	7	4 AAB81354	Aab81354 Tachykin
77	22	100.0	7	4 AAB81431	Aab81431 Tachykin
78	22	100.0	7	4 AAB81420	Aab81420 Tachykin
79	22	100.0	7	4 AAG93350	Aag93350 Aclycal
80	22	100.0	7	4 AAB98845	Aab98845 Chimeric
81	22	100.0	7	5 AAB10085	Aab10085 Substance
82	22	100.0	7	5 ABB09500	Abb09500 Substance
83	22	100.0	7	7 ADE94201	Ade94201 High acti
84	22	100.0	7	7 ADF92529	Adf92529 Substance
85	22	100.0	7	8 ADN95077	Adn95077 Mammalian
86	22	100.0	8	1 AAP20303	Aap20303 Gastroin
87	22	100.0	8	2 AAR28444	Aar28444 Neurokin
88	22	100.0	8	2 AAW57536	Aaw57536 Molecular
89	22	100.0	8	2 AAW52664	Aaw52664 Human tac
90	22	100.0	8	2 AAW92710	Aaw92710 Human tac
91	22	100.0	8	3 AAY67573	Aay67573 P antag
92	22	100.0	8	4 AAB91407	Aab91407 Tachykin
93	22	100.0	8	4 AAB91416	Aab91416 Tachykin
94	22	100.0	8	4 AAB91424	Aab91424 Tachykin
95	22	100.0	8	4 AAG93349	Aag93349 Aclycal
96	22	100.0	8	4 AAB97571	Aab97571 Substict
97	22	100.0	8	5 AAB09498	Abb09498 Substance
98	22	100.0	8	5 ABB09499	Abb09499 Substance

99	22	100.0	8	7	ADB94200	Ad994200 High acti
100	22	100.0	9	1	Ad950634	Ad950634 Substance
101	22	100.0	9	2	Ad972714	Ad972714 Human tac
102	22	100.0	9	4	Ad980325	Ad980325 Human pro
103	22	100.0	9	4	Ad991446	Ad991446 Tachykin
104	22	100.0	9	4	Ad991369	Ad991369 Tachykin
105	22	100.0	9	4	Ad993348	Ad993348 Tachykin
106	22	100.0	9	7	Ad992528	Ad992528 Aclypical
107	22	100.0	9	8	Ad995076	Ad995076 Mammalian
108	22	100.0	10	1	Ad940414	Ad940414 Decapepti
109	22	100.0	10	1	Ad940413	Ad940413 Decapepti
110	22	100.0	10	1	Ad950633	Ad950633 Substance
111	22	100.0	10	2	Ad921933	Ad921933 Substance
112	22	100.0	10	2	Ad965181	Ad965181 S. cerevi
113	22	100.0	10	2	Ad977311	Ad977311 Neurokin
114	22	100.0	10	2	Ad977312	Ad977312 Neurokin
115	22	100.0	10	2	Ad977777	Ad977777 Neurokin
116	22	100.0	10	2	Ad979776	Ad979776 Neurokin
117	22	100.0	10	2	Ad989551	Ad989551 Tachykin
118	22	100.0	10	2	Ad975251	Ad975251 Fragment
119	22	100.0	10	2	Ad974415	Ad974415 HPMBO91
120	22	100.0	10	2	Ad973264	Ad973264 Protein b
121	22	100.0	10	2	Ad969339	Ad969339 Substance
122	22	100.0	10	2	Ad962663	Ad962663 Human tac
123	22	100.0	10	2	Ad982697	Ad982697 Human tac
124	22	100.0	10	2	Ad982698	Ad982698 Human tac
125	22	100.0	10	2	Ad982729	Ad982729 Human tac
126	22	100.0	10	2	Ad982696	Ad982696 Human tac
127	22	100.0	10	2	Ad982728	Ad982728 Human tac
128	22	100.0	10	4	Ad982417	Ad982417 Neurokin
129	22	100.0	10	4	Ad981383	Ad981383 Tachykin
130	22	100.0	10	4	Ad981398	Ad981398 Tachykin
131	22	100.0	10	4	Ad981355	Ad981355 Tachykin
132	22	100.0	10	4	Ad981397	Ad981397 Tachykin
133	22	100.0	10	4	Ad981370	Ad981370 Tachykin
134	22	100.0	10	4	Ad981368	Ad981368 Tachykin
135	22	100.0	10	4	Ad981445	Ad981445 Tachykin
136	22	100.0	10	4	Ad981356	Ad981356 Tachykin
137	22	100.0	10	4	Ad989355	Ad989355 Neurokin
138	22	100.0	10	4	Ad989356	Ad989356 Neurokin
139	22	100.0	10	4	Ad989347	Ad989347 Atypical
140	22	100.0	10	4	Ad984746	Ad984746 Substance
141	22	100.0	10	4	Ad982381	Ad982381 Human neu
142	22	100.0	10	5	Ad982701	Ad982701 Human gen
143	22	100.0	10	5	Ad982715	Ad982715 Human gen
144	22	100.0	10	5	Ad989004	Ad989004 Neurokin
145	22	100.0	10	6	Ad989003	Ad989003 Neurokin
146	22	100.0	10	6	Ad987607	Ad987607 Sea lamp
147	22	100.0	10	6	Ad985028	Ad985028 Human sec
148	22	100.0	10	7	Ad983999	Ad983999 Mosquito
149	22	100.0	10	7	Ad983998	Ad983998 Mosquito
150	22	100.0	10	8	Ad989837	Ad989837 Human sec

ALIGNMENTS

RESULT 1
AAR33009
ID AAR33009 standard; peptide; 5 AA.
XX AAR33009;
AC
XX 25-MAR-2003 (revised)
DT 02-APR-1993 (first entry)
XX
XX Alpha-substituted short peptide.
XX
XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
XX improved bioavailability.
XX Synthetic.
XX

PH Key Location/Qualifiers
FT Modified-site 4
FT FT /note= "alpha-Me-Leu"
FT Modified-site 5
FT FT /note= "Met-NH2"
PN MO9219254-A1.
XX
XX 12-NOV-1992.
PD
XX
XX 15-APR-1992; 92MO-US003119.
PF
XX
XX 24-APR-1991; 91US-00690755.
PR 20-MAR-1992; 92US-00852086.
XX
XX (WARN) WARNER LAMBERT CO.
PA
XX
XX Horwell DC, Hughes J, Richardson RS, Howson W;
PI WPI, 1992-398522/48.
DR
XX
XX New alpha-subst. polypeptide are e.g. selective receptor ligands - for
PT treating inflammation, pain, stroke, ulcers, hypertension, heart failure,
PT depression, cancer, asthma, psychosis, arthritis, etc.
PS Claim 3; Page 41; 46pp; English.
XX
XX
XX The peptide is a specifically claimed example of a group of generically
CC claimed mono-, di-, tri-, tetra- and penta-peptides which include a
CC substituent on an alpha-C atom in the chain. Such substitution may modify
CC the bioavailability, stability or absorbability of the peptide and hence
CC may improve the activity of the peptide as a drug. Depending on the
CC nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic
CC peptide, etc.), the modified peptides are variously useful for treating
CC obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,
CC addictive drug withdrawal symptoms, hypertension, heart failure,
CC cognition or memory disorders, spasticity, depression, diabetes, cancer,
CC asthma, bladder dysfunction, psychosis and arthritis; and as
CC contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on
CC 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 5 AA;
Query Match 100.0%; Score 22; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FPGLM 5
DB 1 FPGLM 5
RESULT 2
AAR33008
ID AAR33008 standard; peptide; 5 AA.
XX
XX AAR33008;
AC
XX 25-MAR-2003 (revised)
DT 02-APR-1993 (first entry)
XX
XX Alpha-substituted short peptide.
XX
XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
XX improved bioavailability.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 2
FT FT /note= "alpha-Me-Phe"
FT Modified-site 5

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:25:34 ; Search time 169 Seconds

(without alignments)
15.150 Million cell updates/sec

Title: US-10-053-669-4
Perfect score: 22
Sequence: 1 FXGLM 5

Scoring table: BLOSUM62DX
Gapop_10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3223

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database: Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	10	1	TKN1_SCYCA
2	22	100.0	10	1	TKN1_CHICK
3	22	100.0	10	1	TKNB_ONCMY
4	22	100.0	10	1	TKNB_RANCA
5	22	100.0	10	1	TKNB_RANRI
6	22	100.0	10	1	TKNC_RANCA
7	22	100.0	10	1	TKNK_PIG
8	22	100.0	10	1	TKNK_RANRI
9	22	100.0	10	1	TKN1_EHYRI
10	22	100.0	10	1	TKS1_AEDAE
11	22	100.0	10	1	TKS2_AEDAE
12	22	100.0	10	1	TKN1_PSEGU
13	22	100.0	10	1	TKN1_PSEIN
14	22	100.0	10	1	TKN1_UPEIN
15	22	100.0	10	1	TKN2_PSEGU
16	22	100.0	10	1	TKN2_PSEGU
17	22	100.0	10	1	TKN2_UPEIN
18	22	100.0	10	1	TKN4_PSEGU
19	22	100.0	10	1	TKN5_PSEGU
20	22	100.0	10	1	TKNA_CAYPO
21	22	100.0	10	1	TKNA_CAYPO
22	22	100.0	10	1	TKNA_CHICK
23	22	100.0	10	1	TKNA_GAMMO
24	22	100.0	10	1	TKNA_HORSE
25	22	100.0	10	1	TKNA_ONCMY
26	22	100.0	10	1	TKNA_RANCA
27	22	100.0	10	1	TKNA_RANRI
28	22	100.0	10	1	TKNA_SCYCA
29	22	100.0	10	1	TKN_ELECT
30	22	100.0	10	1	TKN_PHYFU
31	22	100.0	10	2	Q9UAR8

32	17	77.3	10	2	Q6JL97	Q6J197 neisseria g
33	16	72.7	10	2	Q35013	Q35013 meloidogyne
34	16	72.7	10	2	Q76ML8	Q76ML8 eurypharynx
35	16	72.7	10	2	Q7M278	Q7M278 cricium tu
36	15	68.2	9	1	TRP4_LEUMA	TRP4_LEUMA
37	15	68.2	9	2	Q7M3L3	Q7M3L3 penaeus van
38	15	68.2	10	1	TRP6_LEUMA	TRP6_LEUMA
39	15	68.2	10	1	TRP7_LEUMA	TRP7_LEUMA
40	15	68.2	10	1	TRP8_LEUMA	TRP8_LEUMA
41	15	68.2	10	1	TRP9_LEUMA	TRP9_LEUMA
42	15	68.2	11	2	Q9R446	Q9R446 neisseria g
43	14	63.6	9	1	TKC1_CALVO	TKC1_CALVO
44	14	63.6	9	2	TKL1_LOOMI	TKL1_LOOMI
45	14	63.6	10	2	Q85599	Q85599 moloney mur
46	14	63.6	10	1	TKL2_LOOMI	TKL2_LOOMI
47	14	63.6	10	1	TKL3_LOOMI	TKL3_LOOMI
48	14	63.6	10	1	TKL4_LOOMI	TKL4_LOOMI
49	14	63.6	10	1	TRP5_LEUMA	TRP5_LEUMA
50	14	63.6	11	1	TKC2_CANFA	TKC2_CANFA
51	13	59.1	5	1	TPIS_CANFA	TPIS_CANFA
52	13	59.1	7	1	PPH2_LYCES	PPH2_LYCES
53	13	59.1	8	1	CCRN_DASVI	CCRN_DASVI
54	13	59.1	8	1	CCRN_MACEU	CCRN_MACEU
55	13	59.1	8	1	TXV1_PCONI	TXV1_PCONI
56	13	59.1	8	2	Q94VF3	Q94VF3
57	13	59.1	8	2	Q09258	Q09258
58	13	59.1	9	1	CAER_PHYSA	CAER_PHYSA
59	13	59.1	9	1	CCAP_CARMA	CCAP_CARMA
60	13	59.1	9	1	CCAP_SPOER	CCAP_SPOER
61	13	59.1	9	1	CCAP_TENMO	CCAP_TENMO
62	13	59.1	9	1	FIBB_ERYPA	FIBB_ERYPA
63	13	59.1	9	1	FIBB_MACFU	FIBB_MACFU
64	13	59.1	9	1	FIBB_PAPAN	FIBB_PAPAN
65	13	59.1	9	1	FIBB_PAPAN	FIBB_PAPAN
66	13	59.1	9	1	FIBB_THEGE	FIBB_THEGE
67	13	59.1	9	1	RE42_LITRU	RE42_LITRU
68	13	59.1	9	1	SAMP_MUSCA	SAMP_MUSCA
69	13	59.1	9	2	Q7M3N6	Q7M3N6
70	13	59.1	9	2	Q8M3N1	Q8M3N1
71	13	59.1	9	2	Q8M3N2	Q8M3N2
72	13	59.1	9	2	Q8M3N3	Q8M3N3
73	13	59.1	9	2	Q8M3N4	Q8M3N4
74	13	59.1	9	2	Q8M3N5	Q8M3N5
75	13	59.1	9	2	Q8M3N6	Q8M3N6
76	13	59.1	9	2	Q8M3N7	Q8M3N7
77	13	59.1	9	2	Q8M3N8	Q8M3N8
78	13	59.1	9	2	Q8M3N9	Q8M3N9
79	13	59.1	9	2	Q7M2M7	Q7M2M7
80	13	59.1	9	2	Q67AR4	Q67AR4
81	13	59.1	9	2	Q67AR6	Q67AR6
82	13	59.1	9	2	Q67AR7	Q67AR7
83	13	59.1	9	2	Q67AT1	Q67AT1
84	13	59.1	9	2	Q67AT2	Q67AT2
85	13	59.1	9	2	Q03790	Q03790
86	13	59.1	10	1	CAER_LITXA	CAER_LITXA
87	13	59.1	10	1	DYSE_LITXA	DYSE_LITXA
88	13	59.1	10	1	PRCK_PASHE	PRCK_PASHE
89	13	59.1	10	1	TKU1_UREUN	TKU1_UREUN
90	13	59.1	10	1	TKU2_UREUN	TKU2_UREUN
91	13	59.1	10	1	TPIS_NICPL	TPIS_NICPL
92	13	59.1	10	2	Q7M4X1	Q7M4X1
93	13	59.1	10	2	Q7M4X7	Q7M4X7
94	13	59.1	10	2	Q7M4S2	Q7M4S2
95	13	59.1	10	2	Q25335	Q25335
96	13	59.1	10	2	Q25336	Q25336
97	13	59.1	10	2	Q25337	Q25337
98	13	59.1	10	2	Q6P2D4	Q6P2D4
99	13	59.1	10	2	Q6U014	Q6U014
100	13	59.1	10	2	Q6U015	Q6U015
101	13	59.1	10	2	Q64ET6	Q64ET6
102	13	59.1	10	2	Q6EX62	Q6EX62
103	13	59.1	10	2	Q71VN2	Q71VN2
104	13	59.1	10	2	Q71ZC5	Q71ZC5

105	13	59.1	11	1	RE41_LITRU	P82074 litorea rub
106	13	59.1	11	2	Q9UC46	Q9UC46 homo sapien
107	13	59.1	11	2	Q9TWM2	Q9TWM2 aplysia cal
108	13	59.1	11	2	Q95J19	Q95J19 eulemur ful
109	13	59.1	11	2	Q95J20	Q95J20 eulemur ful
110	13	59.1	11	2	Q95NB6	Q95NB6 eulemur ful
111	13	59.1	11	2	Q77871	Q77871 oreochromis
112	13	59.1	11	2	Q77872	Q77872 oreochromis
113	13	59.1	11	2	Q77873	Q77873 oreochromis
114	13	59.1	11	2	Q70Y64	Q70Y64 plectranthu
115	13	59.1	11	2	Q70Y98	Q70Y98 capitanope
116	13	59.1	11	2	Q8RM18	Q8RM18 enterococcu
117	13	59.1	11	2	Q9CSB3	Q9CSB3 arabidopsis
118	12	54.5	8	1	DYS1_LIMIN	P82079 limodynast
119	12	54.5	8	2	Q83349	Q83349 murine hepa
120	12	54.5	8	2	Q89498	Q89498 murine hepa
121	12	54.5	8	2	Q98RTU5	Q98RTU5 xenopus lae
122	12	54.5	9	1	FARD_CALVO	P41868 calliphora
123	12	54.5	9	2	Q95953	Q95953 homo sapien
124	12	54.5	9	2	Q35953	Q35953 mus musculu
125	12	54.5	10	1	CU30_LOCOMI	P11735 locusta mig
126	12	54.5	10	1	DYS2_LIMDU	P82080 limodynast
127	12	54.5	10	1	PAP1_PARMA	P81863 pardachirus
128	12	54.5	10	2	Q8T688	Q8T688 parietulus o
129	12	54.5	10	2	Q6LCT8	Q6LCT8 rattus norv
130	12	54.5	11	1	PVK1_BLACKR	P83923 blaberus cr
131	12	54.5	11	1	PVK1_BLACKR	P83924 blaptica du
132	12	54.5	11	1	PVK1_GROPO	P83925 gromphadori
133	12	54.5	11	1	PVK1_LEUMA	P83921 leucophaea
134	12	54.5	11	1	PVK1_NAUCT	P83922 nauphoeta c
135	12	54.5	11	1	PVK1_PERAM	P41837 periplaneta
136	12	54.5	11	1	PVK2_BLACKR	P83928 blaberus cr
137	12	54.5	11	1	PVK2_BLACKR	P83929 blaptica du
138	12	54.5	11	1	PVK2_GROPO	P83930 gromphadori
139	12	54.5	11	1	PVK2_LEUMA	P83927 leucophaea
140	12	54.5	11	1	PVK2_NAUCT	P83927 nauphoeta c
141	12	54.5	11	2	Q6UZ55	Q6UZ55 litorea s
142	12	54.5	11	2	Q9TRX0	Q9TRX0 sus scrofa
143	12	54.5	11	2	Q65907	Q65907 silene ajan
144	11	50.0	5	1	ALL2_CARMA	P81805 carcinus ma
145	11	50.0	7	1	ALL2_CARMA	P81806 carcinus ma
146	11	50.0	7	1	ALL3_CARMA	P81807 carcinus ma
147	11	50.0	7	1	ALL4_CARMA	P81808 carcinus ma
148	11	50.0	7	1	ALL5_CARMA	P82158 cydia pomon
149	11	50.0	7	1	ALL7_CYPDO	Q9bry4 homo sapien
150	11	50.0	7	2	Q9BR74	

ALIGNMENTS

RESULT 1
TKNB_SCVCA STANDARD; PRT; 10 AA.
AC P08608;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Scyllorhinus I.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_Taxid=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=6192829; PubMed=2422058; DOI=10.1016/0014-5793(86)80521-X;
RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;
RT "Scyllorhinus I and II: two novel tachykinins from dogfish gut."
RL FEBS Lett. 200:111-116(1986).
RP [2]
RP SEQUENCE.

RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Maugh D., Wang Y., Hazon N., Balmert R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
peptides from the brain of the dogfish, Scyllorhinus canicula."
Eur. J. Biochem. 214:469-474(1993).
RU
CC
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
evolve behavioral responses, are potent vasodilators and
secretagogues, and contract (directly or indirectly) many smooth
muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC
CC PIR; A24867; A24867.
DR InterPro; IPR002040; Tachy Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KM Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.
FT MOD RES 10 10 Methionine amide.
SQ SEQUENCE 10 AA; 1219 MW; D0602D6B59C3AA9 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGLM 5
DB 6 FXGLM 10

RESULT 2
TKNB_CHICK STANDARD; PRT; 10 AA.
AC P19851;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neurokinin A (Substance K) (Neuromedin L).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=88204263; PubMed=2452461; DOI=10.1016/0167-0115(88)90050-X;
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT "[Arg3]ubstance P and neurokinin A from chicken small intestine.";
Regul. Pept. 20:171-180(1988).
RU
CC
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
evolve behavioral responses, are potent vasodilators and
secretagogues, and contract (directly or indirectly) many smooth
muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC
CC PIR; UN0024; UN0024.
DR PDB; 1N6T; NMR; A=1-10.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KM 3D-structure; Amidation; Direct protein sequencing; Neuropeptide;
KW Tachykinin.
FT MOD RES 10 10 Methionine amide.
SQ SEQUENCE 10 AA; 1134 MW; 8A6BA062C9D5BABA1 CRC64;

Query Match 100.0%; Score 22; DB 1; Length 10;

Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXGLM 5
DB 6 FXGLM 10

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OM protein - protein search, using bw model

Run on: October 26, 2005, 08:26:18 ; Search time 37 Seconds
(without alignments)
13.002 Million cell updates/sec

Title: US-10-053-669-4
Perfect score: 22
Sequence: 1 FXGLM 5

Scoring table: FASTA BLAST FASTX
Gapop: 10-0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1328

Minimum DB-seq length: 0
Maximum DB-seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 150 summaries

Database: FASTA BLAST FASTX
1: p1r1:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	10	1	SPPGK
2	22	100.0	10	2	JN0024
3	22	100.0	10	2	B49581
4	22	100.0	10	2	A49581
5	22	100.0	10	2	A24867
6	22	100.0	10	2	S23307
7	22	100.0	10	2	S23386
8	22	100.0	10	2	S07202
9	22	100.0	10	2	G61033
10	22	100.0	10	2	B61033
11	22	100.0	10	2	S27178
12	22	100.0	11	1	A60654
13	22	100.0	11	1	EOCC
14	22	100.0	11	1	EOCC
15	22	100.0	11	1	SPHO
16	22	100.0	11	2	JN0023
17	22	100.0	11	2	S33300
18	22	100.0	11	2	S07203
19	22	100.0	11	2	G60409
20	22	100.0	11	2	E60409
21	22	100.0	11	2	B60409
22	22	100.0	11	2	F60409
23	22	100.0	11	2	D60409
24	22	100.0	11	2	S23308
25	22	100.0	11	2	S23306
26	22	100.0	11	2	S07201
27	22	100.0	11	2	A61033
28	17	77.3	11	2	PT0249
29	16	72.7	10	2	S19296

30	15	68.2	5	2	A61445	Met-enkephalin - b
31	15	68.2	7	2	A60224	Met-enkephalin-Arg
32	15	68.2	9	2	PT0225	Ig heavy chain CDR
33	15	68.2	9	2	PD0027	pev-rachykinin - p
34	15	63.6	4	2	PT0240	Ig heavy chain CRD
35	14	63.6	10	1	ECLQ1M	tachykinin I - mlg
36	14	63.6	10	1	ECLQ3M	tachykinin III - m
37	14	63.6	10	1	ECLQ4M	tachykinin IV - m
38	14	63.6	10	2	S68033	cytochrome P450 1A
39	14	63.6	11	1	ECLQ2M	tachykinin II - m
40	13	59.1	5	2	PT0278	Ig heavy chain CRD
41	13	59.1	6	2	A61049	halo-toxin - Paed
42	13	59.1	7	2	H33098	180K exoantigen -
43	13	59.1	7	2	E33932	Ig mu chain D regi
44	13	59.1	8	2	P00012	cholecystokinin -
45	13	59.1	8	2	A43001	cholecystokinin -
46	13	59.1	8	2	S13661	polygalacturonase
47	13	59.1	8	2	A42057	fibroblast growth
48	13	59.1	8	2	PC4372	telomeric and tetr
49	13	59.1	8	2	A46306	spasmogenic toxin
50	13	59.1	8	2	A61357	phyllotoxin -
51	13	59.1	9	2	D24180	fibrinogen beta ch
52	13	59.1	9	2	C24180	fibrinogen beta ch
53	13	59.1	9	2	E28854	fibrinopeptide B -
54	13	59.1	9	2	F28854	fibrinopeptide B -
55	13	59.1	9	2	D28854	fibrinopeptide B -
56	13	59.1	9	2	S39766	cardioactive pepi
57	13	59.1	9	2	PH0942	T-cell receptor be
58	13	59.1	9	2	S39767	cardioactive pepi
59	13	59.1	9	2	A26363	cardioactive pepi
60	13	59.1	9	2	D57444	neuropeptide Grb-A
61	13	59.1	9	2	S27233	cardioactive pepi
62	13	59.1	9	2	B20569	serum amyloid P-co
63	13	59.1	9	2	S10784	enamelin I - bovin
64	13	59.1	10	2	A61337	caerulein - frog
65	13	59.1	10	2	A13687	caerulein-like pep
66	13	59.1	10	2	H28027	protein p11 - curi
67	13	59.1	10	2	S71948	matrix metalloprot
68	13	59.1	10	2	C39398	Fc mu (IgM) recept
69	13	59.1	10	2	PH0807	T-cell receptor al
70	13	59.1	10	2	A27617	triose-phosphate 1
71	13	59.1	10	2	PN0165	triose-phosphate 1
72	13	59.1	10	2	A59173	nuclease Bhl (EC 3
73	13	59.1	11	2	A33917	dihydroorotase (EC
74	13	59.1	11	2	A35594	buccalin - Callfor
75	13	54.5	5	2	B61445	leu-enkephalin - b
76	12	54.5	9	2	D44787	callfmrinamide 13
77	12	54.5	10	2	A60410	beta-neoendorphin
78	12	54.5	10	2	PT0310	Ig heavy chain CRD
79	12	54.5	11	2	PT0301	Ig heavy chain CRD
80	12	50.0	5	2	G44817	27.5 kda structura
81	11	50.0	5	2	I44817	27.5 kda structura
82	11	50.0	5	2	E44817	27.5 kda structura
83	11	50.0	5	2	E44817	27.5 kda structura
84	11	50.0	5	2	A44817	28K structural pro
85	11	50.0	6	2	PT0643	T-cell receptor be
86	11	50.0	6	2	PT0718	T-cell receptor be
87	11	50.0	6	2	PT0589	T-cell receptor be
88	11	50.0	6	2	PT0727	T-cell receptor be
89	11	50.0	7	2	PT0246	Ig heavy chain CRD
90	11	50.0	7	2	A11483	aspartate transami
91	11	50.0	7	2	PT0663	T-cell receptor be
92	11	50.0	7	2	T09512	NADH dehydrogenas
93	11	50.0	7	2	PT0529	T-cell receptor be
94	11	50.0	7	4	PC2056	trichodecetin I -
95	11	50.0	7	4	PC2057	trichodecetin II -
96	11	50.0	8	2	PT0368	Ig gamma chain C r
97	11	50.0	8	2	PH1618	Ig H chain V-D-J r
98	11	50.0	8	2	PT0627	T-cell receptor be
99	11	50.0	8	2	PT0522	T-cell receptor be
100	11	50.0	8	2	PT0559	T-cell receptor be
101	11	50.0	8	2	PT0554	T-cell receptor be
102	11	50.0	8	2	PT0725	T-cell receptor be

103	11	50.0	8	2	D47393	neuropeptide calla
104	11	50.0	8	4	I55411	hypothetical histo
105	11	50.0	9	2	A61230	caldesquestrin, cat
106	11	50.0	9	2	S65865	collagen alpha 2(V)
107	11	50.0	9	2	PH1591	ig H chain V-D-J r
108	11	50.0	9	2	PS0253	glycine cleavage s
109	11	50.0	9	2	A60356	118k stomach cance
110	11	50.0	10	1	RHPCG	gonadoliberin - pi
111	11	50.0	10	1	RHSHG	gonadoliberin - bh
112	11	50.0	10	1	RHAOL	gonadoliberin I -
113	11	50.0	10	2	PN0136	pepsin (EC 3.4.23.
114	11	50.0	10	2	C45474	chromospondin 2 -
115	11	50.0	10	2	A35556	hypothetical prote
116	11	50.0	10	2	PH1633	ig H chain V-D-J r
117	11	50.0	10	2	PT0632	T-cell receptor be
118	11	50.0	10	2	PT0664	T-cell receptor be
119	11	50.0	10	2	S43630	cytochrome-c oxida
120	11	50.0	10	2	F60527	sperm-activating p
121	11	50.0	10	2	B60589	sperm-activating p
122	11	50.0	11	1	XASNBA	bradykinin-potentl
123	11	50.0	11	2	B58501	24k kidney and bla
124	11	50.0	11	2	S70720	trigger factor hom
125	11	50.0	11	2	PH1670	ig H chain V-D-J r
126	11	50.0	11	2	PH0939	T-cell receptor be
127	11	50.0	11	2	S19775	wound-induced prot
128	11	50.0	11	2	H84082	hypothetical prote
129	10	45.5	4	2	A53284	T-cell receptor be
130	10	45.5	6	2	B56979	collagen alpha 1(I
131	10	45.5	6	2	A41946	T-cell receptor ga
132	10	45.5	7	2	S68004	hucotin, 75k chain
133	10	45.5	7	2	S09066	globulin IV alpha
134	10	45.5	8	2	S63493	disintegrin-like
135	10	45.5	8	2	PA0032	protein QAJ0040 -
136	10	45.5	9	2	S70332	endospem protein,
137	10	45.5	9	2	S70334	endospem protein,
138	10	45.5	9	2	B33098	231k exoantigen -
139	10	45.5	9	2	PT0285	ig heavy chain CRD
140	10	45.5	9	2	PT0670	T-cell receptor be
141	10	45.5	9	2	A56029	N-methylpurine DNA
142	10	45.5	9	2	PC7074	translacion elonga
143	10	45.5	10	1	A61126	gonadoliberin - ap
144	10	45.5	10	1	RHA02	gonadoliberin II -
145	10	45.5	10	2	S10926	inhibin beta-A cha
146	10	45.5	10	2	B46030	gonadoliberin II -
147	10	45.5	10	2	C38925	seed storage prote
148	10	45.5	10	2	B24736	inhibin beta-B cha
149	10	45.5	10	2	I48778	small nuclear ribo
150	10	45.5	10	2	D37397	hypothetical prote

ALIGNMENTS

RESULT 1
SPPGNK
neuromedin K - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
C/Accession: A01560
R/Kanagawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.
Biochem. Biophys. Res. Commun. 114, 533-540, 1983
A/Title: Neuromedin K: a novel mammalian tachykinin identified in porcine spinal cord.
A/Reference number: A01560; PMID:83282812; PMID:6576785
A/Accession: A01560
A/Molecule type: protein
A/Residues: 1-10 <KAN>
A/Cross-references: UNIPROT:P01292
A/Note: The structure of the peptide was confirmed by synthesis
C/Comment: The biological source of this peptide is spinal cord. It stimulates smooth mu
C/Superfamily: neurokinin B precursor
C/Keyword: amidated carboxyl end; hormone; spinal cord
F:/0/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 22; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXGLM 5
Db 6 FVGLM 10

RESULT 2
JN0024
neurokinin A - chicken
C/Species: Gallus gallus (chicken)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: JN0024
R/Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A/Title: [Arg3]substance P and neurokinin A from chicken small intestine.
A/Reference number: JN0023; PMID:8204263; PMID:2452461
A/Accession: JN0024
A/Molecule type: protein
A/Residues: 1-10 <CON>
A/Cross-references: UNIPROT:P19851
C/Superfamily: substance P precursor
C/Keyword: amidated carboxyl end; neuropeptide; tachykinin
F:/0/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 22; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXGLM 5
Db 6 FVGLM 10

RESULT 3
B49581
sialokinin II - yellow fever mosquito
C/Species: Aedes aegypti (yellow fever mosquito)
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C/Accession: B49581
R/Champagne, D.E.; Ribeiro, J.M.
Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994
A/Title: Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito Aec
A/Reference number: A49581; PMID:94105119; PMID:8278354
A/Accession: B49581
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <CHA>
A/Cross-references: UNIPROT:P42635
A/Experimental source: Rockefeller
A/Note: sequence extracted from NCBI backbone (NCBIP:141842)

Query Match 100.0%; Score 22; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FXGLM 5
Db 6 FVGLM 10

RESULT 4
A49581
sialokinin I - yellow fever mosquito
C/Species: Aedes aegypti (yellow fever mosquito)
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A49581
R/Champagne, D.E.; Ribeiro, J.M.
Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994
A/Title: Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito Aec
A/Reference number: A49581; PMID:94105119; PMID:8278354

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OM protein - protein search, using SW model

Run on: October 26, 2005, 08:11:09 ; Search time 162 Seconds

(without alignments)
12.886 Million cell updates/sec

Title: US-10-053-669-4

Perfect score: 22
Sequence: 1 FXGLM 5

Scoring table: BL0SUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 250346

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

Published Applications AA:
1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubppaa/US06_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubppaa/US07_NEW_PUB.pep:*
5: /cgn2_6/prodata/1/pubppaa/PCRS_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubppaa/US08_NEW_PUB.pep:*
7: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
8: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
10: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/prodata/1/pubppaa/US09C_PUBCOMB.pep:*
13: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
14: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
15: /cgn2_6/prodata/1/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
17: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
18: /cgn2_6/prodata/1/pubppaa/US10_NEW_PUB.pep:*
19: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
20: /cgn2_6/prodata/1/pubppaa/US10_NEW_PUB.pep:*
21: /cgn2_6/prodata/1/pubppaa/US60_PUBCOMB.pep:*
22: /cgn2_6/prodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	5	9	US-09-265-690C-1
2	22	100.0	5	9	US-09-265-690C-4
3	22	100.0	5	14	US-10-230-133-4
4	22	100.0	5	14	US-10-053-669-1
5	22	100.0	5	15	US-10-053-669-4
6	22	100.0	5	15	US-10-134-187-3
7	22	100.0	5	16	US-10-688-741-3
8	22	100.0	5	16	US-10-695-536-4
9	22	100.0	5	16	US-10-805-881-1
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Sequence 3, Appl1	;	FILE REFERENCE: 1427001
Sequence 24, Appl1	;	CURRENT APPLICATION NUMBER: US/09/265,690C
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US-09-265-690C-1

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Run on: October 26, 2005, 08:30:04 ; Search time 21 Seconds
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Total number of hits satisfying chosen parameters: 125705

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Post-processing: Minimum Match 0%
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Listing first 150 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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82	22	100.0	10	4 US-09-152-060-110	Sequence 110, App
83	22	100.0	10	6 5169865-11	Patent No. 5169865
84	22	100.0	10	6 5169865-11	Patent No. 5169865
85	22	100.0	11	1 US-07-899-205-1	Sequence 1, Appl
86	22	100.0	11	1 US-07-753-909B-2	Sequence 2, Appl
87	22	100.0	11	1 US-07-934-553-1	Sequence 1, Appl
88	22	100.0	11	1 US-08-184-935-12	Sequence 12, Appl
89	22	100.0	11	1 US-08-269-288-2	Sequence 2, Appl
90	22	100.0	11	1 US-08-338-484-1	Sequence 1, Appl
91	22	100.0	11	1 US-08-175-432-1	Sequence 1, Appl
92	22	100.0	11	1 US-08-462-413-2	Sequence 2, Appl
93	22	100.0	11	1 US-08-225-474-1	Sequence 1, Appl
94	22	100.0	11	1 US-08-391-910-2	Sequence 2, Appl
95	22	100.0	11	1 US-08-418-994-2	Sequence 2, Appl
96	22	100.0	11	1 US-08-480-505-3	Sequence 3, Appl
97	22	100.0	11	1 US-08-391-814-2	Sequence 2, Appl
98	22	100.0	11	1 US-08-167-870-1	Sequence 1, Appl
99	22	100.0	11	1 US-08-428-488-15	Sequence 15, Appl
100	22	100.0	11	1 US-08-428-488-16	Sequence 16, Appl

101	22	100.0	11	1	US-08-428-488-17	Sequence 17, Appl
102	22	100.0	11	1	US-08-255-272-6	Sequence 6, Appl1
103	22	100.0	11	1	US-08-441-591-6	Sequence 6, Appl1
104	22	100.0	11	1	US-08-303-362A-6	Sequence 6, Appl1
105	22	100.0	11	1	US-08-462-859A-1	Sequence 1, Appl1
106	22	100.0	11	1	US-08-123-659A-1	Sequence 1, Appl1
107	22	100.0	11	1	US-08-462-415-2	Sequence 2, Appl1
108	22	100.0	11	1	US-08-463-874-2	Sequence 2, Appl1
109	22	100.0	11	1	US-08-464-247A-1	Sequence 1, Appl1
110	22	100.0	11	1	US-08-464-248A-1	Sequence 1, Appl1
111	22	100.0	11	1	US-08-444-135-2	Sequence 2, Appl1
112	22	100.0	11	1	US-08-318-391-2	Sequence 2, Appl1
113	22	100.0	11	2	US-08-796-598-7	Sequence 7, Appl1
114	22	100.0	11	2	US-08-796-598-11	Sequence 11, Appl1
115	22	100.0	11	2	US-08-496-118-1	Sequence 7, Appl1
116	22	100.0	11	2	US-08-447-175A-7	Sequence 11, Appl1
117	22	100.0	11	2	US-07-737-371E-11	Sequence 15, Appl1
118	22	100.0	11	2	US-07-737-371E-15	Sequence 16, Appl1
119	22	100.0	11	2	US-07-737-371E-16	Sequence 18, Appl1
120	22	100.0	11	2	US-07-737-371E-18	Sequence 19, Appl1
121	22	100.0	11	2	US-07-737-371E-19	Sequence 25, Appl1
122	22	100.0	11	2	US-07-737-371E-25	Sequence 26, Appl1
123	22	100.0	11	2	US-07-737-371E-26	Sequence 33, Appl1
124	22	100.0	11	2	US-07-737-371E-33	Sequence 35, Appl1
125	22	100.0	11	2	US-07-737-371E-35	Sequence 36, Appl1
126	22	100.0	11	2	US-07-737-371E-37	Sequence 37, Appl1
127	22	100.0	11	2	US-07-737-371E-38	Sequence 38, Appl1
128	22	100.0	11	2	US-07-737-371E-38	Sequence 77, Appl1
129	22	100.0	11	2	US-07-737-371E-77	Sequence 1, Appl1
130	22	100.0	11	2	US-08-848-766A-1	Sequence 4, Appl1
131	22	100.0	11	3	US-08-890-157A-4	Sequence 17, Appl1
132	22	100.0	11	3	US-08-927-128-17	Sequence 2, Appl1
133	22	100.0	11	3	US-08-257-966-2	Sequence 1, Appl1
134	22	100.0	11	3	US-09-214-614-1	Sequence 3, Appl1
135	22	100.0	11	3	US-09-265-630C-3	Sequence 2, Appl1
136	22	100.0	11	4	US-08-153-847-2	Sequence 1, Appl1
137	22	100.0	11	4	US-09-635-266-1	Sequence 1, Appl1
138	22	100.0	11	4	US-09-570-022-1	Sequence 5, Appl1
139	22	100.0	11	4	US-09-570-022-5	Sequence 6, Appl1
140	22	100.0	11	4	US-09-570-022-6	Sequence 7, Appl1
141	22	100.0	11	4	US-09-570-022-7	Sequence 8, Appl1
142	22	100.0	11	4	US-09-570-022-8	Sequence 9, Appl1
143	22	100.0	11	4	US-09-570-022-9	Sequence 10, Appl1
144	22	100.0	11	4	US-10-002-593-4	Sequence 1, Appl1
145	22	100.0	11	4	US-09-629-642A-1	Sequence 1, Appl1
146	22	100.0	11	4	US-10-230-133-1	Sequence 21, Appl1
147	22	100.0	11	4	US-09-428-692-21	Sequence 1, Appl1
148	22	100.0	11	4	US-09-285-387A-1	Sequence 1, Appl1
149	22	100.0	11	4		
150	22	100.0	11	4		

ALIGNMENTS

RESULT 1
US-07-753-909B-3
Sequence 3, Application US/07753909B
Patent No. 5304632
GENERAL INFORMATION:
APPLICANT: Vaudry, Hubert
APPLICANT: Conlon, Michael J.
TITLE OF INVENTION: Neuropeptides of the Tachykinin Family
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees, and Sease
STREET: 801 Grand, Suite 3200
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07753, 909B
FILING DATE: 19910903
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9106759
FILING DATE: 04-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Sease, Edmund J.
REGISTRATION NUMBER: 24,741
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515)-288-3667
TELEFAX: (515)-288-1338
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Rana ridibunda
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: brain
US-07-753-909B-3

Query Match 100.0% Score 22; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGLM 5
Db 1 FXGLM 5

RESULT 2
US-07-934-553-2
Sequence 2, Application US/07934553
Patent No. 5314690
GENERAL INFORMATION:
APPLICANT: PATTERSON, ROY
APPLICANT: HARRIS, KATHLEEN E
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGB
NUMBER OF SEQUENCES: 5
TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
CORRESPONDENCE ADDRESS:
ADDRESSEE: TILTON, FALLON, LUNGKUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,553
FILING DATE: 19920821
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: FENTRESS, SUSAN B
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9033CIP
TELECOMMUNICATION INFORMATION:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2005, 08:21:45 : Search time 162 Seconds
(without alignments)
11.937 Million cell updates/sec

Title: US-10-053-669-4
Perfect score: 22
Sequence: 1 FXGLM 5

Scoring table: BLAST2D
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 494136

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Listing first 150 summaries

Database: AA
1: GeneSeq16Dec04:*
2: GeneSeq19908:*
3: GeneSeq20008:*
4: GeneSeq20018:*
5: GeneSeq20028:*
6: GeneSeq20038:*
7: GeneSeq20038:*
8: GeneSeq20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	22	100.0	5 2 AAR33009	AAR33009 Alpha-sub
2	22	100.0	5 2 AAR33008	AAR33008 Alpha-sub
3	22	100.0	5 2 AAR33007	AAR33007 Alpha-sub
4	22	100.0	5 2 AAR33010	AAR33010 Alpha-sub
5	22	100.0	5 2 AAW80134	AAW80134 COOH-term
6	22	100.0	5 2 AAR54549	AAR54549 Cholecyt
7	22	100.0	5 2 AAR54551	AAR54551 Cholecyt
8	22	100.0	5 2 AAR54550	AAR54550 Cholecyt
9	22	100.0	5 2 AAR54548	AAR54548 Cholecyt
10	22	100.0	5 2 AAW41687	AAW41687 Tetrapt
11	22	100.0	5 2 AAW96643	AAW96643 Substance
12	22	100.0	5 2 AAY50325	AAY50325 Neutrophil
13	22	100.0	5 2 AAW92660	AAW92660 Human tac
14	22	100.0	5 3 AAB23028	AAB23028 Mammalian
15	22	100.0	5 3 AAB23025	AAB23025 Human/tac
16	22	100.0	5 3 AAY67576	AAY67576 P antagonist
17	22	100.0	5 4 AAB66674	AAB66674 C-termina
18	22	100.0	5 4 AAB82430	AAB82430 Fluorinat
19	22	100.0	5 4 AAB82431	AAB82431 Fluorinat
20	22	100.0	5 4 AAB81428	AAB81428 Tachykini
21	22	100.0	5 4 AAB70556	AAB70556 Octopus c
22	22	100.0	5 5 AAB10880	AAB10880 Human bet
23	22	100.0	5 5 AAB10088	AAB10088 Substance
24	22	100.0	5 5 AAU77847	AAU77847 Tachykini
25	22	100.0	5 5 AAU77845	AAU77845 Tachykini

26	22	100.0	5 7 ADC64000	ADC64000 Tachykini
27	22	100.0	5 7 ADE94203	ADE94203 High acti
28	22	100.0	5 7 ADF92530	ADF92530 Substance
29	22	100.0	5 8 ADN12180	ADN12180 Tachykini
30	22	100.0	5 8 ADN95078	ADN95078 Mammalian
31	22	100.0	5 8 ADR43774	ADR43774 Mammalian
32	22	100.0	5 8 ADR43771	ADR43771 Human mag
33	22	100.0	6 1 AAP30443	AAP30443 Sequence
34	22	100.0	6 1 AAP40519	AAP40519 Sequence
35	22	100.0	6 1 AAP50694	AAP50694 Sequence
36	22	100.0	6 1 AAP50632	AAP50632 Substance
37	22	100.0	6 1 AAP61486	AAP61486 Peptide h
38	22	100.0	6 2 AAR07897	AAR07897 Cylopept
39	22	100.0	6 2 AAR07893	AAR07893 Cylopept
40	22	100.0	6 2 AAR21959	AAR21959 Substance
41	22	100.0	6 2 AAR27696	AAR27696 Cyclic ta
42	22	100.0	6 2 AAR27694	AAR27694 Cyclic ta
43	22	100.0	6 2 AAR27695	AAR27695 Cyclic ta
44	22	100.0	6 2 AAW9686	AAW9686 Substance
45	22	100.0	6 2 AAW92706	AAW92706 Human tac
46	22	100.0	6 2 AAW92659	AAW92659 Human tac
47	22	100.0	6 2 AAY31052	AAY31052 Non-cross
48	22	100.0	6 3 AAY67575	AAY67575 P antagonist
49	22	100.0	6 4 AAB82453	AAB82453 Fluorinat
50	22	100.0	6 4 AAB82432	AAB82432 Fluorinat
51	22	100.0	6 4 AAB82436	AAB82436 Fluorinat
52	22	100.0	6 4 AAB82433	AAB82433 Fluorinat
53	22	100.0	6 4 AAB81421	AAB81421 Tachykini
54	22	100.0	6 4 AAB81425	AAB81425 Tachykini
55	22	100.0	6 4 AAB81419	AAB81419 Tachykini
56	22	100.0	6 4 AAG93951	AAG93951 Aclypical
57	22	100.0	6 4 AAB74306	AAB74306 Peptide a
58	22	100.0	6 4 AAB98884	AAB98884 Chimeric
59	22	100.0	6 4 AAB98886	AAB98886 Chimeric
60	22	100.0	6 5 AAB10087	AAB10087 Substance
61	22	100.0	6 5 AAB10086	AAB10086 Substance
62	22	100.0	6 6 AAB37288	ABJ37288 Rhodopsin
63	22	100.0	7 1 ADE94202	ADE94202 High acti
64	22	100.0	7 1 AAP20310	AAP20310 TYR8-SP5-
65	22	100.0	7 2 AAR21956	AAR21956 Substance
66	22	100.0	7 2 AAR21957	AAR21957 Substance
67	22	100.0	7 2 AAW29539	AAW29539 Aap-Ser-P
68	22	100.0	7 2 AAY50324	AAY50324 Neutrophil
69	22	100.0	7 2 AAW92662	AAW92662 Human tac
70	22	100.0	7 2 AAW92705	AAW92705 Human tac
71	22	100.0	7 3 AAY67574	AAY67574 P antagonist
72	22	100.0	7 4 AAB80323	AAB80323 Human pro
73	22	100.0	7 4 AAB80324	AAB80324 Human pro
74	22	100.0	7 4 AAB82428	AAB82428 Fluorinat
75	22	100.0	7 4 AAB82429	AAB82429 Fluorinat
76	22	100.0	7 4 AAB81354	AAB81354 Tachykini
77	22	100.0	7 4 AAB81431	AAB81431 Tachykini
78	22	100.0	7 4 AAB81420	AAB81420 Tachykini
79	22	100.0	7 4 AAG939350	AAG939350 Aclypical
80	22	100.0	7 5 AAB98845	AAB98845 Chimeric
81	22	100.0	7 5 AAB10085	AAB10085 Substance
82	22	100.0	7 5 ABB09500	ABB09500 Substance
83	22	100.0	7 7 ADE94201	ADE94201 High acti
84	22	100.0	7 7 ADF92529	ADF92529 Substance
85	22	100.0	7 8 ADN95077	ADN95077 Mammalian
86	22	100.0	8 1 AAP20303	AAP20303 Gastroint
87	22	100.0	8 2 AAR28444	AAR28444 Neurokin
88	22	100.0	8 2 AAW57536	AAW57536 Molecular
89	22	100.0	8 2 AAW52664	AAW52664 Human tac
90	22	100.0	8 2 AAW92710	AAW92710 Human tac
91	22	100.0	8 3 AAY67573	AAY67573 P antagonist
92	22	100.0	8 4 AAB81407	AAB81407 Tachykini
93	22	100.0	8 4 AAB81416	AAB81416 Tachykini
94	22	100.0	8 4 AAB81424	AAB81424 Tachykini
95	22	100.0	8 4 AAG93939	AAG93939 Aclypical
96	22	100.0	8 4 AAB97571	AAB97571 Substicuc
97	22	100.0	8 5 ABB09498	ABB09498 Substance
98	22	100.0	8 5 ABB09499	ABB09499 Substance

99	22	100.0	8	7	AD894200	Ad894200 High acti
100	22	100.0	9	1	AAp50634	AAp50634 Substance
101	22	100.0	9	2	AAw92714	AAw92714 Human tac
102	22	100.0	9	4	AA880325	AA880325 Human pro
103	22	100.0	9	4	AA891446	AA891446 Tachykin
104	22	100.0	9	4	AA891369	AA891369 Tachykin
105	22	100.0	9	4	AA899348	AA899348 Atypical
106	22	100.0	9	7	ADf92528	ADf92528 Substance
107	22	100.0	9	8	ADN95076	ADN95076 Mammalian
108	22	100.0	10	1	AAp40414	AAp40414 Decapepti
109	22	100.0	10	1	AAp50633	AAp50633 Substance
110	22	100.0	10	2	AA821933	AA821933 Substance
111	22	100.0	10	2	AA821933	AA821933 Substance
112	22	100.0	10	2	AA85181	AA85181 S. cerevi
113	22	100.0	10	2	AA877311	AA877311 Neurokin
114	22	100.0	10	2	AA877312	AA877312 Neurokin
115	22	100.0	10	2	AAW79777	AAW79777 Neurokin
116	22	100.0	10	2	AAW79776	AAW79776 Neurokin
117	22	100.0	10	2	AAW48951	AAW48951 Tachykin
118	22	100.0	10	2	AAW5251	AAW5251 Fragment
119	22	100.0	10	2	AAW74415	AAW74415 HPMBQ1 p
120	22	100.0	10	2	AAy23264	AAy23264 Protein b
121	22	100.0	10	2	AAy06939	AAy06939 Substance
122	22	100.0	10	2	AAW92663	AAW92663 Human tac
123	22	100.0	10	2	AAW92697	AAW92697 Human tac
124	22	100.0	10	2	AAW92698	AAW92698 Human tac
125	22	100.0	10	2	AAW92729	AAW92729 Human tac
126	22	100.0	10	2	AAW92696	AAW92696 Human tac
127	22	100.0	10	2	AAW92728	AAW92728 Human tac
128	22	100.0	10	4	AA882417	AA882417 Neurokin
129	22	100.0	10	4	AA881383	AA881383 Tachykin
130	22	100.0	10	4	AA891398	AA891398 Tachykin
131	22	100.0	10	4	AA891355	AA891355 Tachykin
132	22	100.0	10	4	AA891397	AA891397 Tachykin
133	22	100.0	10	4	AA891370	AA891370 Tachykin
134	22	100.0	10	4	AA891368	AA891368 Tachykin
135	22	100.0	10	4	AA891445	AA891445 Tachykin
136	22	100.0	10	4	AA891356	AA891356 Tachykin
137	22	100.0	10	4	AA899355	AA899355 Neurokin
138	22	100.0	10	4	AA899356	AA899356 Neurokin
139	22	100.0	10	4	AA899347	AA899347 Atypical
140	22	100.0	10	4	AA864746	AA864746 Substance
141	22	100.0	10	4	AA882381	AA882381 Human neu
142	22	100.0	10	5	AA827017	AA827017 Human gen
143	22	100.0	10	5	AA827155	AA827155 Human gen
144	22	100.0	10	5	AA899004	AA899004 Neurokin
145	22	100.0	10	5	AA899003	AA899003 Neurokin
146	22	100.0	10	6	ABG76074	ABG76074 Sea lamp
147	22	100.0	10	6	ABU65028	ABU65028 Human sec
148	22	100.0	10	7	ADc63999	ADc63999 Mosquito
149	22	100.0	10	7	ADc63998	ADc63998 Mosquito
150	22	100.0	10	8	ADg89837	ADg89837 Human sec

ALIGNMENTS

RESULT 1
 AAR33009 standard; peptide; 5 AA.
 ID AAR33009;
 AC AAR33009;
 XX 25-MAR-2003 (revised)
 DT 02-APR-1993 (first entry)
 XX Alpha-substituted short peptide.
 XX CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
 KM improved bioavailability.
 OS Synthetic.

PH	Key	Location/Qualifiers
FT	Modified-site	4 /note= "alpha-Me-Leu"
FT	Modified-site	5 /note= "Me-NH2"
XX	MO9219254-A1.	
PN	12-NOV-1992.	
PD	15-APR-1992;	92WC-US003119.
PF	24-APR-1991;	91US-00690755.
PR	20-MAR-1992;	92US-00852086.
XX	(WARN) WARNER LAMBERT CO.	
PA	Horwell DC, Hughes J, Richardson RS, Howson W;	
PI	WPI; 1992-398522/48.	
DR	New alpha-subst. polypeptide are e.g. selective receptor ligands - for	
XX	treating inflammation, pain, stroke, ulcers, hypertension, heart failure,	
PT	depression, cancer, asthma, psychosis, arthritis, etc.	
PS	Claim 3; Page 41; 46pp; English.	
XX	The peptide is a specifically claimed example of a group of generically	
CC	claimed mono-, di-, tri-, tetra- and penta-peptides which include a	
CC	substituent on an alpha-C atom in the chain. Such substitution may modify	
CC	the bioavailability, stability or absorbability of the peptide and hence	
CC	may improve the activity of the peptide as a drug. Depending on the	
CC	nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic	
CC	peptide, etc.), the modified peptides are variously useful for treating	
CC	obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation,	
CC	addictive drug withdrawal symptoms, hypertension, heart failure,	
CC	cognition or memory disorders, spasticity, depression, diabetes, cancer,	
CC	asthma, bladder dysfunction, psychosis and arthritis; and as	
CC	contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on	
CC	25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR	
CC	field.) (Updated on 25-MAR-2003 to correct PI field.)	
XX	Sequence 5 AA;	
SQ	Query Match	100.0%; Score 22; DB 2; Length 5;
	Best Local Similarity	80.0%; Pred. No. 1.8e+06;
	Matches	4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 FPGLM 5	
DB	1 FPGLM 5	
RESULT 2		
AAR33008		
ID AAR33008 standard; peptide; 5 AA.		
XX	AAR33008;	
XX	25-MAR-2003 (revised)	
DT 02-APR-1993 (first entry)		
XX	Alpha-substituted short peptide.	
XX	CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;	
KM	improved bioavailability.	
OS	Synthetic.	
XX	Key	Location/Qualifiers
FT	Modified-site	2 /note= "alpha-Me-Phe"
FT	Modified-site	5